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From:

Sent:

Slobodyansky, Elizabeth Wednesday, July 31, 2002 11:44 AM STIC-Biotech/ChemLib

To: Subject:

09/900,038

Please search for case 09/900,038:

SEQ ID NOs: 1 and 2 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652 CM1 10D11 703-306-3222

mail box 10C01

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SUMMARIES

Result Query No. Score Match Length DB ID Description

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(E-mail:miyake@proc.nubio.nagoya-u.ac.jp, Tel:81-52-789-4278,
Fax:81-52-789-3221)
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us-09-900-038a-2.rge

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AF337958 16448 bp DNA linear BCT 27-FEB-2001 Streptococcus agalactiae strain NT6 type VI capsular polysaccharide synthesis operon, complete sequence.
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McKinnon, K., Chaffin, D.O. and Rubens, C.E.
Direct Submission
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895. .2425

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Streptococcus agalactiae
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AUTHORS
TITLE
JOURNAL
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RBS gene CDS	gene RBS CDS	gene RBS CDS	RBS gene CDS

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LYFRIGSKMDKC"
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                                                                                                                                                             Score 363.4; DB 1
Pred. No. 8.5e-47;
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9965. .10913
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62.4%;
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Matches 585;
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Methanococcacee; Methanococcus.

(bases 1 to 1456)

(co.J., White,0., Olsen,G.J., Zhou,L., Fleischmann,R.D., Sutton,G.G. Blake,J.A., FitzGerald,L.M., Clayton,R.A., Gocayne,J.D., Kerlavage,A.R., Dougherty,B.A., Tomb,J., Adams,M.D., Reich,C.T., Overbeek,R., Kirkness,E.F., Weinstcock,K.G., Merrick,J.M., Clodek,A., Scott,J.D., Geoghagen,N.S., Weidman,J.F., Fuhrmann,J.L., Nguyen,D.T., Utterback,T., Kelley,J.M., Peterson,J.D., Sadow,P.W., Hanna,M.C., Cotton,M.D., Hurst,M.A., Roberts,K.M., Kalne,B.B., Borodovsky,M., Klenk,H.P., Fraser,C.M., Smith,H.O., Woese,C.R. and Venter,J.C.

Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

Science 273 (5278), 1058-1073 (1996)
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Bult.C.J., White,O., Olsen,G.J., Zhou,L., Fleischmann,R.D.,
Bult.C.J., White,O., Olsen,G.J., Zhou,L., Fleischmann,R.D.,
Sutton,G.G., Balake,J.A., FitzGerald,L.M., Clayton,R.J.,
Gocayne,J.D., Kerlavage,A.R., Dougherty,B.A., Tomb,J.-F.,
Adams,M.D., Reich,C.I., Overbeek,R., Kirkness,E.F., Weinstock,K.G.,
Meritck,J.M., Glodek,A., Scott,J.D., Geoghagen,N.S., Weidman,J.F.,
Fuhrmann,J.L., Nguyen,D.T., Utterback,T. K. Kelley,J.M.,
Peterson,J.D., Sadow,P.W., Hanna,M.C., Cotton,M.D., Hurst,M.A.,
Roberts,K.M., Kaine,B.B., Borcodovsky,M., Klenk,H.P., Fraser,C.M.,
Smith,H.O., Woese,C.R. and Venter,J.C.
Direct Submission
L. Submitted (27-Aug-1996) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
On Jan 30, 1998 this sequence version replaced gi:1591709.
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TVHPSAMVKSKILKKIYDEKLIRSQDYDFWIRCIANDYKFDIIEEFLLKYRIPNRDN
YLSRIKKQKLYSYTLKTHWKNKKHFCNNVYFWKVFFYSLVVYLFIVLFPFILKILI
                                                                                                                                                                                                                                                                                                                                                                       linear BCT 28-JAN-1998 of the complete genome.
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   tatatttatactttaagtctcccttggttaggaggttattaataataatgatattaatattt
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/db_xref="taxon:2190"
184. .1056
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Methanococcus jannaschii section 91
U67549 L7117
U67549.1 GI:2826363
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184. .1056
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1067. .2896
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NETALFELEHELNSEK IRCFIGDVRDKDRLKRA I EEVDVVFHAAALKHVPLCEYNPFE
AVKTNY IGTONLIEVAMDEEVEKFTI I STDKAVNPWARTKLAERLTI SANLYKG
KRYAFSVYNFGVVLNSRGSILDLLKEQIKKGGPYLTHPDMTRFINSINEAVKLVLK
ACYLAKGGEIFILKMESVRIKDLIEVVIEELAPKOGYRPEDIEIK II GKRPGEKLYEE
LII I EEEI YNLEELEDMFVVY PYGVDGNKNNKII YNSKDAKFLNKEKIKKILKEISYL"
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LKRYSKSDK KIYKNIDNMAELMKDNDLITTSPGMTWFEALFLGIPVVVLQVBELQRE
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NTIRKVGSVNVSQLNTDNPFIGILIGEFFLWGKHIGRHSVSLVLKWLKNIGYKKAHAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"MKIIGIIQARTGSKRLKNKVLLKLGDRCILEILLERLKKSKKLD
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/product="spore coat polysaccharide biosynthesis protein F
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HYDKKHIRKYDSSTIIKSGTLLRPVBIAARGMKIIGBENFGEPFVERVERDGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MKIAIITDGSVEWGMGHVYRTLSLANELRKFNVNEIIFFTKSDE
DVIKKIEENGFKVIKCSDNNDILKNIKNIKPDVVIIDDLGIEEDFAKNIRELCKKLIF
FDNPNPSSNKYADIVVNAIVGSELKNRKYFDEENKTLYFYGPKYLILRNEFYKVKKEM
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                                                                                                                                                                                                                                                /note="similar to GB:X73124 SP:P39627 PID:413993 pe. identity: 32.60; identified by sequence similarity; putative"
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GB:AL009126 percent identity: 38.94; identified b
sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             G, putative (spsg)"
/protein_id="AAB99065.1"
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/gene="MJ1062"
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complement(8936. .9580)
/gene="MJ1064"
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Best Local Similarity
Matches 365; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            KIQRLAMAGGVVANVIMNLNIFERTPFEELYIFPAMGDDĞVAAGAAILKAVELGEDIS
WLKDLEMPYKGPNYSREDVRELKKDKWKDKITYEYIGEKRPEIAARATAKGNIIAVY
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VINTSFNLHGRTIVRTPEDAITDFIDCNIDAMFIEGYLVKRKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKNNNYRFDILETTDYDRYYGNNRFGGNHLFKNEEFKKLLKNFDINLTDKNYSILFTK
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RFLYWKYPKKEKTILFVSQGYPEFYELIFNTFRDKKLINTLIEHGYSFYFKPHPGEY
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                                                                                                                                                                                                                                                                                                                              YEHHLCHAASAYYFSPFFPKETLVFTLDGIGDWKYHSLWLFKEYDYRLVSYSSFDIIC
                                                                                                                                                                                                                                                                                                                                                         YDDVEGIFKGASIGHIYSLFTEILGFTPNSDEGKTEALAAYGKPNGELYNLLKKGYKI
                                                                                                                                                                                                                                                                                                                                                                                 NK EKLRWEHDINILKKLHNKQYLQKWKEK IGDENFAATIQRWLEDTVVEYLNIVY EKF
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protein_id="AAB99064.1"
/db_aref="GI:1591713"
/translation="MPQDISNPYKDKTILVTGGTGSIGKEIVKTLLKFNPKTIRVLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:U10927 SP:P39862 PID:506709 percent identity; 31.91; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"capsular polysaccharide biosynthsis protein M"
/protein_id="AAB99063.1"
/db_xref-"GI:1591712"
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/protein_id="AAB99072.1"
                                 /note="similar to PID:1653353 percent identity: 35.19;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4130. 5743 // Agene="MJ1060" // Anote="Mypothetical protein; identified by GeneMark; putative"
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by sequence similarity;
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/db_xref="GI:1591711"
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/gene="MJ1061"
complement(5738. .6739)
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                                                                                                                                                   /product="nodulation
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putative"
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/transl_table=11
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4130, 571
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/gene="MJ1059"
2913. .4133
/gene="MJ1059"
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4130. .5743
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                              'note="similar
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Coyne, M.J. and Comstock, L.E.
Direct Submission
Submitted (07-JUL-2000) Channing Laboratory, Brigham & Women's
                                                                                                                  atcaaacgettactgattttgagttcataattgtcattgataatccaagtagaggtgatt 136
                                                                                                                                                                                                                                 257 atatttttagaatggatgctgatgatatttcatatccaagtagatttgataagcaaattc 316
                                                                                                                                                                                                                                                                                                                                                               581 AAAATGGAAATAT----TTTAAAAGAGTTTAAGCCCAGAAAAATATAAATTTAAAGAAA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                         494 aagttttegataagttaatgggatatagagatttagtacetgttgaagattatgattttg 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A conserved Region of the Bacteroides fragilis Chromosome Upstoof the Polysaccharide B Locus Contains Genes Implicated in the
221 TAATGGCAACATACAACGAACCAGAAAAATATTTAAAGGAATCTATTGAGTCAATTTYAA 280
                                                                                                                                                                                                401 AAAGAAATTTAGGTAGAGGGGCCAGTAGAAATAAAGCTGTTAATATAGCAAGGGGGAAGT 460
                                                                                                                                                                                                                                                                                                 317 gttttatggaggaaaattca---ttggatttctcagcaactctaatagaattgatagacc 373
                                                                                                                                                                                                                                                                                                                                695 AAATCTTAAAGAAATTAAAATACGATGAGAAATTAATTAGGTCTCAAGACTACGATTTTT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caataagaagagctctggctgatttcaaaatcggcttactcaataaagtacttttacagt 613
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Bacteroides fragilis NCTC 9343 PS B capsular polysaccharide
                                                tanagcaattettaacagaatatteagttgtagataatagaataaaaatettgettaatg
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Coyne,M.J., Kalka-Moll,W., Tzianabos,A.O., Kasper,D.L. and
Comstock, L.E.
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Coyne, M.J. and Comstock, L.E.
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Bacteroides fragilis
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/protein_id="Abdise00.sc"
//protein_id="Abdise00.sc"
//db_xref="G1:18152899"
//db_xref="G1:1815289"
//d
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/db_xref="GI:18152897"
/translation="MKKIILVAALLSAAVCLPAQNKGGNKSGGINLSLWKKACTQPLD
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SNVNGNNLAGLSVSGLVNITGNKAKGVLITGLSNIAGDNMRGLMMSGIMNITGDKAAG
VQLAGLANTYGEEYDGLMMSGLLNVVGEEMNGLQLSGLANTYGGOMNGVQLGLFNFAS
KKGLQIGLFNYKKEDMKGLQLGLVNNNPQTKVQLMYFGGNSTKINVGARFKNKLFYT
ILGGGTHYLDFDDKFSAALFYRAGLEDLYRNLFVSGGNSTGNHTFRNKKVBGIPAR
LYALQARLNLEYRFTDKFGLFVRGGLEDLYRNLFVSGDIGYQHIETFRNKKVBGIPAR
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IFEESGIRKGDKIAVCGRNSSHWGVTFLATLTYGAVIVPILHEFKADNVHNIVNHSEA
KLLFVGDVVWENLNESAMPLLEGILMMNDFTLLVSRSERLTHAREHLNEMFGKKFPKN
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VSMLDMAHWCGLAFEFLYEFAGCOJYFLTRNPSPK I IFQFAFDVKPKIJVAVPLI IE
KI IKKSVLPKLETPTWKLLLKVP I INDK IKATVREEM IKGFGGNFEAVIVGGAARNQE
VEQFLEMIDFPYTVSKOFFCGPI I CYEDWKRFKFGGSGRAALNMEVKVLSPDEBVV
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SGONIYPEEIEDKLNNLPYVAESIIVQONDKLVGLVYPDFDEAFAHGLKNEDMERVME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(222. .1379)
/note="Orfl; Glycine- and asparagine-rich protein with a large number of clustered repeats; similar to putative pentose-5-phosphate 3-epimerase (PPE) protein from Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                  181 Longwood Avenue, Boston, MA
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                                                                                                                                                                                                                                                                       Laboratory, Brigham & Women's
                Boston,
                                                                                                                                                                                                                                                                                                                                                                                                                   update by submitter
5, 2002 this sequence version replaced gi:11023503.
Location/Qualifiers
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complement(3340. .4422)
/gene="fc1"
Hospital/Harvard Medical School, 181 Longwood Avenue,
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/product="GDP-4-keto-6-deoxy-D-mannose-3,
5-epimerase-4-reductase"
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/rransl_table=11
/product="unknown
/protein_id="AAL61889.1"
/db_xref="GI:18152898"
                                                                                                                                                                                                      Direct Submission
Submitted (16-MAR-2001) Channing
                                                                                                                                                                                                                                                                                                       Hospital/Harvard Medical School, 02115, USA
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/organism="Bacteroides
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/db_xref="taxon:817"
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                                                     02115, USA
4 (bases 1 to 34508)
Coyne, M.J. and Comsto
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On Jan 15,
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/transl_table=11

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VMDNLHVSEYWMPFTTGLLVYPVMLLCSWLLNOIPAPNEQDIIOFTKRAPMDGKDRRK
FLROFFWGICMLVVFYGALTYFREIADSFAADIWKELHIEGAMIFTGTEVPIAAFVLV
IMELIVFVRNNRLALNIIYCLAVTGGSLMVFSTLLIVVGFLSPIWWMILSGLGLYMGY
IPFTYLIERLIASLHVVSTAVFIIXAADSFGYLGTTGVFMVKNFVSADISWTVMLMRT
ALFSGFVSVLSIFAIXCYFKQQLNSLLIPSEHD"
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                                                                                                                                                                                                                            /translation="MIRSFLSRSPLYVLALYASVLIFLVYTCAYAYRKPFTAAIYEGE
                                                                                                                                                                                                                                                    ILWGFDVKILYVLSEIIGYALSKFIGVRILPSMKAGHRIYYIIGLLTFSEVALLGFAL
LPVPLKVCSIFLSGLPLGMIWGVIFSYIEGRRISEILNVGLSVALIVSSGLVKTLGQF
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [ (bases I to 14157) Nolling,J., Breton,G., Omelchenko,M.V., Markarova,K.S., Zeng,Q., Gibson,R., Lee,H.M., Dubois,J., Qiu,D., Hitti,J., Wolf,Y.I., Tatusov,R.L., Sabathe,F., Doucette-Stamm,L., Soucaille,P., Daly,M.J., Bennett,G.N., Koonin,E.V. and Smith,D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22262 AAGATTAGCGTATTGATGTCTATATAAAGAGAATTCTCTTTATGTAAGACAAGCTATT 22321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22382 GAAGATTTTATTTTAGATAAGTTTAGAAATAGCAAGAAAAGATAGTGTATACAA 22441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22442 TATCAACGAAATGAAAAAATATAGGTTTAGCAGCCACTTTGAATCGTCAGATTTGTGTA 22501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 atcttgcttaatgaagaaaatattggtttagcatcaagtttgaacaaagcggtgaaaatt 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 agtagaggtgatttaaagcaattcttaacagaatattcagttgtagataatagaataaaa 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 gaatctatattaaatcaaacgcttactgattttgagttcataattgtcattgataatcca 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/protein_id="AAG26464.1"
/db_xref="G1:11023507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE007717 14157 bp DNA linear BCT 27-JK Clostridium acetobutylicum ATCC824 section 205 of 356 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 aattatagtatcattatgtcggtatataaatgagcctttaaattatgtgagagattcagta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 34508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 120.8; DB 1
Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22562 ATTATGCAGGTTGAATACTTAGATAGAAATAC 22593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gataagcaaattcgttttatggaggaaaattc 335
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Clostridium acetobutylicum.
                                                                                                                           /transl_table=11
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AE007717 AE001437
AE007717.1 GI:15025159
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="wcfU"
11754. 12473
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                                                                                                   /codon_start=1
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                                                .11761
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10478. .11767
                                                                     /gene="wcfT"
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60.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.99
Best Local Similarity 60.27
Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE007717/c
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E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MATTYDGINYFPIAVNFWEENAMEVIEAKYGMKGLAIVLKLLCK
IYKEGYYIPWGEEQCLIFANKTGKEADAEEVQGIIEIMIEKGMIDRGSYAEHKVLTSE
SIQKWIEARTRRKRNWTAMPYLLIKRKETCNREEKTYCTQUNEQDAGSDAKINCONTEQ
SKYKGSREFPPSAPPRGFEEVNATPVSMFCYAFNTTHNYVGLMGNLERFGITDEKE
IEALIKLSDYGRKGTPWKLLCSTNWSNIGAKGKYMIAALNRAKKRSGT"
complement(8120. .8467)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVSFEIFPFSFSEHRILERVEATGKNYAETMCKGALPILENLEPDAEAGWKAISALRDT
ILFRDIIRRYRIKDARLLEDVFVYLCTHLAELITIGGLVSHPAAGNRKTSYDTVANYI
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ELRRAGYTVFVGVGGKLVDFVGRKKDRIYYLQCAPLLNDDFGVEGMYNTLEMIQDN
YEKWVVSMDDTTLPSKEGIRHIQVWQLPEIL
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TLYGMLDARKDWGYAKDYVECHWLILQHDVPEDFVIATGEMHTVREFCTLAFAEIGIN
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/gene="upby"
9468. .9992
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/gene="upb2"
9996. .10481
                                                                                                                                                                                                                                                  5702. .6973 /note="Orf3"
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/gene="upbY"
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/gene="upb2"
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EELEKEVTARIPIRTNRDDRYTTNYYOGLPLDGYTKMFENMLMHENIHIMLNTDYKFI
KSEIQYKSLIYTGCADEFFPYKFGRLPYRSINFEFFTLNQDYYQKVGTVNYPNDYDFT
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DKIIMCNVISEFKDRDRLSIYIMELSSFVFKILSGFFTCLFGIVSVPFLIFKLRAAKK
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ISFLKSHRÜIDILGYÖVKVVGUISNDIKEKRENKLIPEEDIYDDNREKILNYWCLAH
PSVMFRKÜILRELKGYNDFKSEDLDLAMLRAIESGFKIYKLKEELLYFRMHEESKTRVD
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DKFKTGEFEKIRILHPKDINHIKFDYVFIATEPGKEEAMSSLKSMGLKCIKDFLSTV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Glycosyltransferase"
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complement(6689. .8038)
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/codon_start=1
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/db_xref-"GI:15025164"
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                                                                                                                                                                                                                                                                                                                                                                         complement(5153. .5638)
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Childress, D., Zeng, Q. and Smith, D.R.
Direct Submission
Submitted (24-JUL-2001) GTC Sequencing Center Production,
Finishing, and Bloinformatics teams, Genome Therapeutics Corp., 100
Beaver Street, Waltham, MA 02453-8443, USA
Location/Qualifiers
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DTYNNINSFSEGVQQAESDIRDSDVADEMITYTKTGVLMNAGDAMLAQANQLPKDILN
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   Genome Sequence and Comparative Analysis of the Solvent-Producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Nucleoside-diphosphate-sugar epimerase"
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Bacteriol. 183 (16), 4823-4838 (2001)
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MEDLINE
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AUTHORS
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1 (bases 1 to 3584)
van Der Wel, H., Morris, H.R., Panico, M., Paxton, T., North, S.J.,
Dell, A., Thomson, J.M. and West, C.M.
A Non-Golgi alpha 1, 2-Fucosyltransferase That Modifies Skpl in the Cytophasm of Dictyostelium
J. Biol. Chem. 276 (36), 33952-33963 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF279134 3584 bp DNA linear INV 05-SEP-20 Dictyostellum discoideum alphal, 2-fucosyltransferase (fucB) gene, complete cds; and unknown genes.
8638 ATTTATGATGATAATAGAGAAAAAATATTAAATTATTGGTATTGTTTAGCACATCCTTCA 8579
                                                                                                                                                                                                                                                                                      8402
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                                                                                                                                                      gaagattatgattttgcaataagaggagctctggctgatttcaaaaatcggcttactcaat 597
                                                                                                                                                                                                                                                                   caatattttactcagctattttacaagatttttataaagaaaaatcttatattgatatc
                                                                                                                                                                                                                                                                                                                                                                          8401 TATGAAGGTTTAAAAGATGGAATAAAAATAAAATTAATAGATGTTTTTAAGAGAGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                        acaaaaattactaattactttcaagagtatgtgataaagaaacgctatactcagcaagag
                                                                                                        GTAATGTTTAGGAAAGATATTTGAGAGGCTAAAAGGATACAATGATTTTAAATC---A
                                                                                                                                                                                                                                          aaagtacttttacagtatagattaaacgagaatggaatatcacaaaccaataagtttaag
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1. .3584
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van der Wel, H. and West, C.M.
Direct Submission
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32610-0235, USA
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VERSION
KEYWORDS
SOURCE
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TITLE
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EVENKNKDVDILACKYVEAFGDVSREGKLEREHWYNVDLNNSESIESLFLENCYIAHPS
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GFI DKY KEGEV DECRIY KPEDLMKLHSDY VFIATLPGKEEADEFLKNCGLKKFK FY I S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MISVIMPVYNCEKYLEESIESILKQTYRDFEFIIVNDGSNDKSI
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0; Mismatches 440; Indels
                                                             /product="Glycosyltransferase"
/protein_id="AAK80132.1"
/db_xref="G1:15025168"
                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Glycosyltransferase"
/protein_id="AAK80133.1"
/db_xref="G1:15025169"
                                                                                                                                                                                                                                                                                                        /gene="CAC2175"
complement(10149. .11150)
/gene="CAC2175"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAK80134.1"
/db_xref="G1:15025170"
                                                                                                                                                                                                                                                                                      complement(10149. .11150)
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                    /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="CAC2176
                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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al Similarity 50.1%;
467; Conservative
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Extremophiles 3 (3), 227-233 (1999)
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HORINGSHI, K. TSUJII;
249-284; Springer-Verlag (1999)
(sites)
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Extremophiles 3 (1), 29-34
99184646
8 (sites)
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Bacillus halodurans genc
AP001519 BA000004
AP001519.1 GI:10176109
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DEFINITION
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NTTSAFSPRVYSISS(SSNGSISSMSSMMMMSGGNQPLIGSPSEMIMHKLKE
IERLNKBAIQKDQELNQVKKIABABRSRLCLLKDKYKEVRNELIEKELVK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAF82379.1"
/db_xref="GI:9022427"
/translation="DPTKENNTVGHVVKQGYRLHDRLVRPAMVGVNKIKPQ"
442 c 365 g 1290 t
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                                                                                                                  /product="alphal,2-fucosyltransferase"
<1067. ..>3373
/gene="fucB"
1067. ..3373
                                                                                                                                                                                                                                                                               /codon_start=1
/product="alphal,2-fucosyltransferase"
/protein_id="AARB2378.1"
/db_xref="GI:9022426"
                                                                                                                                                                                                                                                            /note="glycosyltransferase
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/gene="fucB"
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Makasone,K., Hirama,C., Takaki,Y., Masul,N., Fujl,F.,
Nakamura,Y. and Inoue,A.
An improved physical and genetic map of the genome of alkaliphillic
Bactilus sp. C-125
Extremophiles 3 (1), 21-28 (1999)
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Masui, N., Fuji, F., Takaki, Y., Inoue, A. and Horikoshi, K.
Sequencing of three lambda clones from the genome of alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125 Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)
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Takami,H.
Genome analysis of facultatively alkalihilic Bacillus halodurans
                                aaaatatacttaactaatgatatacggaagatgttattgaatagatctatacttgcccac 471
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Takami, H., Masui, N., Nakasone, K. and Horikoshi, K.
Replication origin region of the chromosome of alkaliphilic
Bacillus halodurans C-125
Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takami, H. and Horikoshi, K. Reidentification of facultatively alkaliphilic Bacillus sp. to Bacillus halodurans
Biosci. Biotechnol. Biochem. 63, 943-945 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki,R., Hirama,C., Fuji,F. and Masui,N.
Genetic analysis of the chromosome of alkaliphilic Bacillus
halodurans C-125
                                                                                                                        ccaacgtggtgcgtaaaaaagaaagttttcgataagttaatgggatatagagtttagta
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Takami, H., Takaki, Y., Nakasone, K., Hirama, C., Inoue, A. and
Horikoshi, K.
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halodurans genomic DNA, section 13/14.
BA000004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus halodurans DNA.
Bacillus halodurans
Bacteria; Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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2 (sites)
Takami, H., Takaki, Y., Nakasone, K., Sakiyama, T.,
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IRRSVDFWANYGGTFICLPTASIQASIGASIGTYMGLVEVGVGVIPGGGGKKELY
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YQAKQQVIHLHDAGYRPPARKKIPVVGETGYATMLLGAKSMKFGGMISEHDLKIAEKL
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6030. .6353
/gene="BH3490"
/note="BH3490
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/gene="BH3489"
5746. .6015
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6761. 7150
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/gene="BH3492"
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unknown"
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RTEKAIRRNGLEKAAEQKLALTQVFCQGAFNRIEAHAKESLVAMGSGDTLRTWTSILRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (122-MAR-2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group; 2-15 Natsushima, Yokosuka, Kanagawa 237-0061, Japan (E-mail:takamih@jamstec.go.jp, URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html, Tel:81-468-67-3895, Fax:81-468-66-6364)

1. 303650
                                                                                                             9 (sites)
Nakasone,K., Masui,N., Takaki,Y., Sasaki,R., Maeno,G., Sakiyama,T.,
Hirama,C., Fuji,F. and Takami,H.
Characterization and comparative study of the rrn operons of
alkaliphilic Bacillus halodurans C-125
Extremophiles 4 (4), 209-214 (2000)
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VSREDQDAFAVESHKRAAKAIEEGKFADEIVPVDVTLGHVDDHKLVBEHVTESVDEG
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SFAVAGVAPEIMGVGPVEAIPKAVKMAGLDLSDIGLFELNEAFASQAIQVIRGLNLDH
DKVNVNGGAIALGHPLGCTGTKLTLSLIHEMKRRGEQFGVVTMCIGGGMGAAGVFELI
                                                                                                                                                                                                                                                                                                                                                                                                                      Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28 (21), 4317-4331 (2000)
Analysis of the genome of an alkaliphilic Bacillus strain from an
                                                                                                                                                                                                                                                                                                                                         Takani,H., Nakasone,K., Takaki,Y., Maeno,G., Sasaki,R., Masui,N.,
Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and
Horikoshi,K.
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                             industrial point of view Extremophiles 4 (2), 99-108 (2000)
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Takami, H. and Takaki, Y.
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Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
   3;
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For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Nor ke sequence is in progress and the release of this data is based on the understanding that the
                                                                                                                                                                                                                                                                           245969 TCTAATAATTAATGATGCTTCTACTGATGGAAGTGG---GGAATTGCTAGAGGAATACTC 245913
                                                                                                                                                                                                                                                                                                                                                                                                                      245674 AGAAAGGTACCAACTACACATAGG----GAGATTGCTAATTTAATATGGACTTGCCCTTT 245619
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
I (bases I to 67970)
Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M. and Barrell, B.
                                                                                                                                               246029 AAATTATTTAAGCGAAAGTATAGAAAGTATCCTAAACCAAACATTTGAAAACTTTGAGTT 245970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245792 TGTTTCATTTAAAGACCGTCTTGCTGTTCAAATGGATCATGTTAAGGCCCACTCA--GAA 245735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tatticatatccaagtagatitgataagcaaaticgtittaiggaagaaaattcatigga 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agaaagtaataaaatatacttaactaatgatatacggaagatgttattgaatagatctat 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tttctcagcaactctaatagaattgatagaccaaaaaggaaatttagtatataaaacaacg 401
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                                                                           aaattatgtgagagattcagtagaatctatattaaatcaaacgcttactgattttgagtt 101
                                                                                                                                                                                                                               cataattgtcattgataatccaagtagaggtgatttaaagcaattcttaacagaatattc 161
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   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agatttagtacctgttgaagattatgattttgcaataagaggagctctggctgatttcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acttgcccacccaacgtggtgcgtaaaaaaaaaagtttcgataagttaatgggatatag
                                                                                                                                                                                                                                                                                                                                                                              agttgtagataatagaataaaaatcttgcttaatgaagaaaatattggtttagcatcaag
   6
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281; Indels
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Plasmodium falciparum MAL1P3, complete sequence.
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1. .67970
/organism="Plasmodium falciparum"
   Mismatches
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   Conservative
Matches 299;
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PFMAL1P3
LOCUS
DEFINITION
ACCESSION
VERSION
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JOURNAL
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SOURCE
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/strain="3D7"

source

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/translation="MKLVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV
LQIKKRSNIKKNHNIRKMEDNESSFIDIGSNLTDKWEDGGYNSKKHENDLQNYLNRAK
NINVDKIIITCTCLAEIDKSLKICETYDPEGKRIYLSAGVHPTNCYEFIDKNKHEEKE
IITAKKEYEEFIXYFKNEQVENSKMENGNKKLCDGEKDMNINBILLEKNLDTIPGFKY
NEKDKEYLENLKKIIKYPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIFQLKLVQMFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLKDRLNKKEEIKFTSIIMPLYVYKILISNVANFPNLVNNVMBGIVNIKRLNNYINDH
LYYNDIKNYPMYRNYNNINVONTFELQMENITSHDDGTSHULKHLKNVIKNKTN
KYFPFYKMYNHNIINKOILSGLLKNVDDNTNKKICFQEHKSNSTYNYNSSHIHE
MFKEYFFYNIHNSCAWNENERFEKSINDYIIKLENDFOLGYDNKONDHILKNINPN
LKRNSLAIIIGNVGSGKSAFFHSILGDFNMTHGNLYIENFFKKMPILYVPQNSWLPMG
                                                                                                                                 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPMFLHMRNCSETFFKIVDIYKFLFEKNGGVIHSFTDKEDIVHIIVQNYKNLYIGVNG
CSLKSLENINAVKKIPLNLLLETDAPWCGVKKTHASYEYIKDTYEKRAYTNLKKIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:6594245"
/translation="MKLLNNRFVVLCPIIILFFFLNSVVLGNNNRNNINFHETENAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMRKLLSGETNSTKLDNGDELKIKLNDEKHKDSTKWDKSYSFISNLEEEKYSQTDLFR
KKQEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTTYRENVGISNKGNKKKKSCQNISFLNFLSFDWIRPLINDLIK
GDIQELPNICRNFDVPYYASKLEENLRDIEVEDSEFYSEKNSSNEHVLHHCNSNDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKVYNYYYHNILMSIIKTFKRRIILIISFYILETLIYTLGGKFIDYYMFILEGOKIPV
YISFLKDFKVFSGLVVVMIMFFHLFFEALLHFYFHLFTINLKVSLMYFLYKINLCSNN
NHLQNPDAFYNTYRKFSSQTEIDEISRDFLSIGKNASSSSSGIKNNKNIDNNKFVEN
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MSFYVFHIKIGSNSVGIAIMLSIALYSAMILFEFLPSLFKSKYLIYRDKRIDNMHHVL
KEFKLIKMFNWESFAFKYINIFRMKEMKYCKIRLYLSNIGVFISSISSDIVEVVIFFI
                                                                                                                                                                                                                              aa
                                                                                                                                                                                                                                                                                                              /product="conserved hypothetical protein, UPF0006 family"
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/db_xref="G1:6594244"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8020. .10389
/note="possible cen1, region of very high [A+T] content"
14884. .20152.
/gene="MALIP3.03"
/gene="MALIP3.03"
/note="MALIP3.03"
/codon_start=1
                                                                                                                       /note="MALIP3.01, conserved hypothetical protein, len: aa, similarity: UPF0006 family eg to YBL0552/YBL0512/YBL0511, YBF5_YEAST (418 aa), fasta scores: opt: 316, E(): 1.1e-12, (33.2% identity in 271 overlap)"
      .3276))
                                                                  .3276))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="potential splice donor sequence, aaa/gtaaaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein, len: 163
      .2598,2748. .2848,2990.
                                                                  .2598,2748. .2848,2990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"hypothetical protein, MAL1P3.02"
/protein_id="CAB63557.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="potential splice acceptor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="potential splice acceptor sequence"
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/protein_id="CAB63558.1"
/db_xref="GI:6594246"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MAL1P3.02, hypothetical pro
contains possible signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="potential splice donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2599. .2610)
/gene="MAL1P3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2742. .2747)
/gene="MAL1P3.01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2849. .2861)
/gene="MAL1P3.01"
complement(join(1748.
/gene="MALIP3.01"
complement(join(1748.
/gene="MALIP3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIKCDDNTIFKERNEPYNIA"
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/gene="MAL1P3.02"
5005. .5496
/gene="MAL1P3.02"
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/db_xref="G1:6594247"
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RFKRITARASEDOKYWWEEDFCLILNEEE1.RPEHNDSPVLPEHYBNIDK.NELSINS
TRYMKETITKMRQNYEKETDNNNHNWRDFWHYKWANIYLYKVHKLINITLKDLTNPI
HDKEFITTWTKWIDDDIEFFLDNLYFWNLYLYKWEI.
complement(32477. .32486)
/gene="MAL1P3.04"
                                                                                                                                                          YTLDTYTSNNSDKEEIVKPLYKDTHEEFNKSSSMPFVKSSSNMINNPSNFKYEDNSSS
FKGSISLETYLWYFQQVGFVLLTSVVIFMLISIFTDEIKFVFLTMMSIISKNNKEHSD
TILOKQVYKLEFYVLEDIISLATSGICFSMIIYGNITSAIKVHNNILYSILNAPLYIF
YNNLGNIINFFIIDISAFDYGFLKRIYRAFFIFFCILSSLLIIYMINDCIFIFPFV
ILLIYFFVFRRPSGCKRAPLACHTPLCNIYSNALSGKNIINIYKKNTYHLDVYF
HYINNFRISYFFKWLINIWASLYIKIFILLLTTYIIMHPHLYASGIIKLYKEKNYVRI
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Cfnysidrslaegssesketkvkdipniellkslninyeeyekmkeivgsfmdnnnln
Ianevlknihsftnienifslindsskspvlktflkefgsifphmlnnvpkllfdlco
                                                                                                                                                                                                                                                                                                                                                                                                                   KKIPLVNGTYKYIDEEPSLKNINMYALKNOKIGIVGKSGAGKSTILLSILGLINISOG
STYDERDIPTYNRKGEBSITGILAGSSFYFYNMYIRTFIDPDPYNHFYDDEIVHALKLN
GINLGKNDLYKYMHQDMKSNYKKIIQTSKYINQSNOWTILLTNOCIRYLSLYRLYLN
RHKYKIILLIDEIPIFNLNNSVHDELNSFLIGKAKSFNYIIRNHFPNNTVLIISHHANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MALIP3.04, conserved hypothetical membrane protein, len: 203 aa, similarity: P. falciparum chromosome 2, prep110w, 096126 predicted integral membrane protein (255 aa), fasta scores: opt: 335, E(): 4.9e-15, (36.1% identity in 191 aa overlap)"
RALYEHYIHMHKLCTDYEKKLIQPNEILDKDLINNKNISSYNNKKSKLVNYNIPFNEN
YLQKCLMDDNNFYLYLLDDIFTSLDPSISKKIFSNLFCKEDNISFKDNCSFIISMNKS
                                                                                              IDYTRIKLFDEVELNHVKHSNKMIYKERYFVKGNTESVSFEIDSINKEYIKKMKKNY
KKEHMNKNNKDNNNNNNNSNKDDHININMNDNHRNYNDINLGPNSTDDSPTVSSLGNE
                                                               TLDNFLIEDILDNVQY EVNIFEIQDKTLKYRGNISEYMEKNNLNITKESHWGY SNLNT
                                                                                                                                                                                                                                                                                                                                                       LSTLGYCISFSARLGVIIKFLLCDYTHIEKEMCCVQRLEEFAKISNKENASMNKENEL
NVITTQTYKEKNENISDKISAIVEYKNVSLSSIINSSQDDESKKKYGIKFENVYVSYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"MAL1P3.06, garp, len: 673 aa, similarity: almost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="region containing small subunit, 5.8S and large subunit rRNA genes and spacer regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="potential splice donor sequence, aaa/gtatat"
| join(36657. 36743,36864. .37343)
| join(36657. .36743,36864. .37343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="potential splice donor sequence, aag/gtatga"
36854. .36863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="conserved hypothetical membrane protein, MAL1P3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MAL1P3.05, hypothetical protein, len: 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23896. .31533
/gene="rRNA"
complement(foin(31966. .32476,32675. .32775))
/gene="MALIP3.04"
/gene="MALIP3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .40284))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="potential splice acceptor sequence"
complement(32669. 32674)
/gene="MALlP3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein, MAL1P3.05"
/protein_id="CAB63560.1"
/db_xref="GI:6594248"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="potential splice acceptor sequence" complement(join(38049. .39995,40210. .4028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSCCDYIYVLRKGEITYRCSYEDVKTQSELSHLLEMDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(38049. .39995,40210.
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/gene="MAL1P3.05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MAL1P3.05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23896. .31533
/gene="rRNA"
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                                                                                                                                                                                                              /translation="MNVLFLSYNICILFFYVCTLNFSTKCFSNGLLKNQNILNKSFDS
ITGRLLNETELEKNKDDNSKSETLLKEEKDEKDDYPTTSNDNLKNAHNNNEISSSTDP
TNIINVNDKDNENSVDKKKDKKEKKHKKDKKEKKEKKDKKEKKDKKEKKHKK
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aa), fasta scores: 97.6%
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join(45401. 46396,46562. .50233)
/gene="MALIP3.07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cagttgtagataatagaataaaaatcttgcttaatgaagaaaatattggtttagcatcaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acceptor sequence"
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                                                                                         /protein_id="CAB63561.1"
/db_xrefe="G1.65".1"
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Pred. No. 3.9e-05;
0; Mismatches 424;
identical to GARP_PLAFF (678
                                     identity in 678 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(39996. .40005)
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Best Local Similarity 47.5%;
Matches 395; Conservative
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Consensus quality: 33034 bases at least Q30
Consensus quality: 33034 bases at least Q30
Consensus quality: 33871 bases at least Q30
Estimated insert size: 36477; sum-of-contigs estimation
Quality coverage: 6.56 in Q20 bases; sqarose-fp estimation
Quality coverage: 7.73 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a "working draft' sequence. It currently
* consists of 6 contigs. The true order of the pleces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                               DNA linear HTG 03-JUL-2001
LLNLFOS-20C5, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 36977)
DOE Joint Genome Institute.
                                                                                                                               701 aatettatattgatateacaaaaattaetaattaettteaagagtatgtgataaagaaae
                                                                                              761 gctatactcagcaagagctctctaaatattttgagctaaaatctacccctagtattacta
                                                                                                                                                                                 9326 TAACATTATAATAAAATATATATATATATAATAAATTAATATTATTA 9376
                                                                                                                                                                821 ttagaaaactatatatttgtttatattttatactttaagtctcccttggtta 871
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contig of 2068 bp in length
contig of 2222 bp in length
contig of 2222 bp in length
gap of unknown length
contig of 7465 bp in length
contig of 9216 bp in length
contig of 9216 bp in length
gap of unknown length
gap of unknown length
contig of 13926 bp in length
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                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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Center clone name: LLNL-FOS_20C5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing of Human Chromosome 19
                                                                                                                                                                                                                                                                                AC092304 36977 bp
Homo sapiens chromosome 19 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                 SEQUENCE, 6 unordered pieces.
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gap of
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36977: contig
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DOE Joint Genome Institute.
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Pred. No. 0.0015;
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Best Local Similarity 46.7%;
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TCSFILVILLDMIYEGRIGAVESELTIFAYIVTFFDLSKIFNKKTFILLFIVVIALVNA
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1138. . .2223
1138. .2223
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Wang, L., Ou, W. and Reeves, P.R.
Direct Submission
Submitted (25-JUL-2001) Department of Microbiology, The University of Sydney, Sydney, NSW 2006, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 10911)
Wang, L., Qu, W. and Reeves, P.R.
Sequence Analysis of Four Shigella boydii O-Antigen Loci:
Implication for Escherichia coli and Shigella Relationships
Infect. Immun. 69 (11), 6923-6930 (2001)
                                                                                                                                                                         AF402315 11near BCT 04 Shigella boydii serotype 9 O-antigen gene cluster, partial
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Shigella boydii
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8961

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312

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Y07786.1 GT:2244680
galactosyltransferase; mannose-1-phosphate guanylyl transferase;
ORF21x9 gene; ORF34x7 gene; ORF35x9 gene; ORF39x2 gene; ORF40x0
gene; ORF40x1 gene; ORF41x3 gene; ORF41x8 gene; ORF41x9 gene;
ORF50x8 gene; ORF54x5 gene; ORF56x5 gene; oxido-reductase; Rfc-11ke
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2 (bases 1 to 16265)
Stroeher,U.H., Parasivam,G., Dredge,B.K. and Manning,P.A.
Novel Vibrio cholerae 0139 genes involved in lipopolysaccharide biosynthesis
J. Bacteriol. 179 (8), 2740-2747 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Manning, University of Adelaide, De
ly, GPO Box 498, Adelaide S A 5005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9202 AAAGATGCATTTGATGATATAA---AAATGCCATTAATTAGGACTGGTCAAGATTATGCG 9258
                         gatttaaagcaattettaacagaatatteagttgtagataaaaaaaaatettgett 192
                                               attcgttttatggaggaaaattca...ttggatttctcagcaactctaatagaattgata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                cagtatagattaaacgagaatggaatatcacaaaccaataagtttaagcaatatttac
                                                                                                      aatgaagaaaatattggtttagcatcaagtttgaacaaagcggtgaaaatttctaaggga
                                                                                                                                          8902 AACCCAGTAAATTCTGGTGCGGCAGTTTCCAGAATAATTCACTAAAAATGCCAATGGG
                                                                                                                                                                                                                            8962 GAATITATIGCTITCCTIGATAGCGATGATITGTGGGAGGCATCTAAACTIGAAAAACAA
                                                                                                                                                                                                                                                                                                           9022 ATATTATGGATGCTGAAAAATCCAAATATAACATTCTCATTTACAGCATATGAACTTATT
                                                                                                                                                                                                                                                                                                                                                        gaccaaaaaggaaatttagtatataaacaacgagaaagtaataaaatatacttaactaat
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                                                                                                                                                                                                                                                                                                                                                                                                                                     aagaaaagttttcgataagttaatgggatatagaagtttagtacctgttgaagattatgat
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V.cholerae ORF's involved in lipopolysaccharide synthese.
Y07786 Y07787
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/organism="Vibrio cholerae"
/strain="AI-1837"
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1 (bases 1 to 16265)
Manning, P. A.
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Vibrio cholerae
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AUTHORS
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NKIKKAKRQWEIYRKIEGLPLVYSVICFISYGWRAIFRR"
                                                                                                                                                                                                                                                                                 NIKNEYVIFVILVAXRCMVELLSIFFIKNKVOLSKIRLKFSSGINAIKKTYSYALFOI
SSSIYLYGLSLIASIVIDKNIIIYHLLAERVEKLASFFFSQATRVIYSFLNNFTGNNK
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GIMSVSGFLTKGNIKYLNVTIIIAGCVSIPVCYFLSSSYPQISTSIAYVVAEGLISLI
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                                                                                                                                                                                                                                             SFATWVAIVIEFGENYSSAKQIKYDSNKVKVISVINSTLSAKIILSLLAIILGIYTSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8728 ATTATTATGCCTGCGTATAATTCGCAGT----ATACAATAAAAGATACTATACAATCTGTT 8784
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/FSSMLKFSKKYNKQLDFILYYIGVSFSYFFKKPSYALLRLRAMNFRLNK"
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                                                                                                                                                                                                                                                                                                                                                                         LLIKFVPELLKENKYESREDNIK"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="RmlC"
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/transl_table=11
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/gene="rmlC"
8163.
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/gene="gnd"
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/gene="gnd"
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/gene="wbgs"
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                                                         6944. .8191
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                                                                                                /note="Wzx"
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SVVFIQFEQYESIAEYSFIVUSSIALITHGULINATUNINSRYKFTYAAUITLEIGLII
SVVFIQFRQTAMAMIYGLAFSQIFFSVILYNIITSEQEFSIVKIKSAFNKHYMKGVLF
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5379. 6395
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ENCFIDKRFLSYEDLYSYMKEMSDEEYIGYINNIQAFLKSDLSSPFRAETFAEKVVS
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IYNPKYFFYFNGLKFIAFNQLYRMKSNRDEVKDRNDCKMMESLIENNQYKNIKAKKK
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Direct Submission
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Escherichia coli serotype 055:H7 O-antigen gene cluster, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8934 AGCAAACATTTCTGATTTTGAATTTATTATTATCATTAATGACGGTTCGAC-----TGATA 8987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mang,L., Huskic,S., Cisterne,A., Rothemund,D. and Reeves,I
The O-antigen gene cluster of Escherichia coll O55:H7 and
identification of a new UDP-GICNAc epimerase gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 8.2%;
al Similarity 57.2%;
183; Conservative
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Escherichia coli
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13211. .14617
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Pred. No. 0.0026;
0; Mismatches 213; Indels 12;
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TEXQTPLATE CONTROLLER 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MCCTDLLFRLRSPFKICRSPIKKRAWSFITSRGWLTLAAAISGH
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complement[1377...14266]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MYQSIHASLARNVFVKTSPRLFSTPLCQCVALMTSSLLTSSLLV
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HYALDSRSAIAFDFINHANGDEARLNTVNLSFQLKF"
                                                                                                                                                                                                                           YSDQASFSGDTKYTDKSIDAKLRLMQESYWLPELSLGLRDIGGTGLFDGEYLVATKQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(13577..14266)
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complement(12711. .13577)
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15645. .18380
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14935. .15525
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Yamasaki,S., Shimizu,T. and Hoshino,K.
Direct Submission
Submitted (14-APR-1998) Shinji Yamasaki, Internatinal Medical
Center of Japan, Research Institute: Toyama 1-21-1, Shinjuku, Tokyo
162-8655, Japan (E-mail:shinji@ri.imcj.go.jp, Tel:+81-3-3202-7181,
Fax:+81-3-3202-7364 (24-Sep-1998).
Sequence updated (24-Sep-1998).
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TAYERTNODYLQNLESFKRRATNALGSLGGEIDLDIIDQRDTPWTVPSDVELSSAQLF
VDGKQFNAPYAYLWQSLNTSSBDXYSYSNLINDVNYYLKLKCKEISPPSSPYWKPQHV
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SELTVPSGLPIFIKQTIYSPYHNELPVMKFDSPILDQELKEIRDFSVSWIKTPSSSIT
ETFLYQYQDLYKRTLGSELIDPSIDNIPLLKNISAQQDQDLLKRQPYTWWLEE"
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YCLDREIPFLYASSAATYGETDTFIEEPQYEGALNVYGYSKQQFDNYVRRLWLDAKQH
DETLSOITGFRYRWYGPREQHKGSMASVAFHLNNQNNAGENPKLFAGSENFKRDFVY
VGDVAAVNLWFLDHGVSGIFNCGTGKAESFNEVAKAVIAFHGRGEVETIPFPDHLKGA
YQEFFEADLTKLRAAGCDVQFKSVAEGVAEYWALINRK"

COMPLEMENT (8924. . 10441)
                                                                                                                                                                                                                       AB012956 46721 bp DNA linear BCT 16-OCT-1999 Vibrio cholerae genes for O-antigen synthesis, strain MO45, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YamasaKii, Shimizu, T., Hoshino, K., Ho, S.T., Shimada, T., Nair, G.B. and Takeda, Y.
The genes responsible for O-antigen synthesis of vibrio cholerae 0139 are closely related to those of vibrio cholerae 022 (Gene 237 (2), 321-332 (1999)
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Db 12172 TCAAAATTTACCGGAATATTTATTCTATTACAGGTTGCATGA 12213
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/gene="gmhD"
/note="probable LPS core synthesis"
/codon_start=1
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complement(7866. .8810)
/gene="gmhD"
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COMMENT

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AC106820.1 GI:18139370
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WGGIIDFGNARLDFLKRYGHFBAGIPSADTLSRVMGMINPVALQRSFIAWMKNCHTLT
DGEVIAIDGKTLRGSYDRSKGKGTIHWVNAFATANGMSIGQLKVDSKSNEITAIPKLL
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PROSSSYSTORGKEHGRIEFRVALVNRDLSVLGDIEHEWPGLKSMGIVASIRQESAVATE
QDVSIRYYIGSKELEAQYLLEATRSHWGVEWHWSLDTAFCEDNSRIRADDRAEAFAR
IRQICLNLLKSETTFKGGIKRKRMNCAMDEKYLSKVLESLT"
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LEVPPFRNTISIMGEVQVPYTYLLDSGLNVDDYLNKAGGVKKQADADRIFVVRADGSV
YKPNSGVWFGNNKEKLQAGDTIVVPIDTDYRDALSTWTAATQILYQTGVAINALK"
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/db_xref="G1:372430
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'note="probable transport of capsular precursors"
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/codon_start=1
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Pred. No. 0.0023;
                                                                                                                                  /protein_id="BAA33592.1"
/db_xref="G1:3724303"
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/note="
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/gene="IS1358"
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/gene="IS1358"
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chamically treated genomic DNA (Homo saptens)-original length of seq 1: 3.67378 <223>-split as follows.-seq 01 0.000.001 70 0.349.980-seq 02 0.300.001
1.249.980-seq 03 600.001 949.980-seq 04 900.001
1.249.980-seq 05 1.200.001 1.1549.980-seq 06 1.500.001
2.449.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001
2.449.980-seq 07 1.800.001 2.749.980-seq 10 2.700.001
3.049.980-seq 11 3.000.001 3.673.78 <223>-original length of seq 2: 3.673778 <223-split as follows.-seq 18 1.200.001
1.549.980-seq 19 10.500.001 1.849.980-seq 18 1.200.001
2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001
2.749.980-seq 22 3.700.001 3.649.980-seq 26 3.600.001
3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001
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44.6%; Pred. No. 0.002;
iive 0; Mismatches 423;
 68007 AATATATCTAATTATGGATATTATATATATAAT 67973
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Olek,A., Piepenbrock,C. and Berlin,K.
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Sequence 6 from Patent WO0200932
AX344555 AX344555.1 GI:18492441
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                                                                                                                                                                              Length 177509
                                                                                                               others
                                                                                                                                                                              Score 77; DB 2; Length 177
Pred. No. 0.0018;
0; Mismatches 460; Indels
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Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

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/db.xref="taxon:7227"
/clone_libb="RPCI-98"
/clone=BACR08K10"
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                                                                                                                                                                Drosophila melanogaster genome survey sequence T7 end of BAC: BACKS9B23 of RPCT-98 library from Drosophila melanogaster (fruit AL069706
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="texon:7227"
/clone_lib="RPCI-98"
/clone="BACR29B23"
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Conservative 105; Mismatches 310;
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B11336 F19W10-Sp6 IGF Arabidopsis thaliana genomic clone F19W10, DNA thale cress. Arabidopals thaliana Exabidopals: thaliana Exabidopals: Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Eukaryota; Viridiplantae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida, II; Brassicales; Brassicaceae; Arabidopsis. Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and /note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI; Produced by Thomas Altmann" 47 others Dept. of Biology, University of Pennsylvania, Philadelphia, PA 19104 aaatcggcttactcaataaagtacttttacagtatagattaaaacgagaatggaatatcac 640 557 556 TTTAAATTATWTTTTTTTTAWTAWAWWTWAAAWAATWAWWWWAAAATWWWWTTTT 497 aaaccaataagtttaagcaatatatttactcagctattttacaagatttttataaagaaa aatcttatattgatatcacaaaaattactaattacttcaagagtatgtgataaagaaac ttagaaaactatatatttgtttatatttatactttaagtctcccttggttaggaggttat gctatactcagcaagagctctctaaatattttgagctaaaatctaccctagtattacta DB 12; Length 1248 1. 1248 /organism="Arabidopsis thaliana" Score 71.6; DB Pred. No. 0.015; Fax: 215-898-8780 Email: jecker@atgenome.bio.upenn.edu Seq primer: Sp6 Arabidopsis Thaliana Genome Center High quality sequence start: 102 High quality sequence stop: 138. Location/Qualifiers taataaatgatattaatatttagtactg 909 TWATTWATAAWTTTWTTTWWAWATTWWKK 468 /db_xref="taxon:3702" /clone_lib="IGF" /sex="hermaphrodite" /strain="Columbia University of Pennsylvania BAC End Sequences at ATGC /clone="F19M10 7.68; Unpublished (1997) Other_GSSs: F19M10-T7 B11336.1 GI:2092456 1 (bases 1 to 1248) Tel: 215-898-9384 Class: BAC ends Contact: Ecker

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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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    . cycganism="Drosophila melanogaster"
/plasmid="pBeloBACil"
/db_xref="taxon:7227"

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Collaboration with the Berkeley Diosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fultifly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Goegawa and Aaron Mammosar in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecoli digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 1919 19006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
GSS 04-JUN-1999
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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/clone_lib="RPCI-98"
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- Web : www.genoscope.cns.fr)

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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="Exxon:7227"
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Centre National de Sequencage: Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr )
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton pBelobAcl1.
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                                                                                                    10;
                                                                      Length 1101;
              others
                                                                     Query Match 7.3%; Score 68.2; DB 12; Length Best Local Similarity 31.1%; Pred. No. 0.056; Matches 276; Conservative 160; Mismatches 441; Indels
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Delymorphisme Humain) with funding provided by a MRC and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        622
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Pterrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1001)
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                      BAC
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Drosophila melanogaster genome survey sequence SP6 end of BACN11B06 of DrosBAC library from Drosophila melanogaster fly), genomic survey sequence.
AL103554
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Pred. No. 0.082;
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GSS 26-JUL-1999
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence T7 end of BAC BAC BACILILII of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL104216
AL104216.1 GI:5615827
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                                                                                                                                        815 ttactattagaaaactatatatttgtttatatttatactttaagtctcccttggttagga 874
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                                                                                       ATAWTTAAAWTWTTAAAWTTAAATAAATWTATTTAAAATWTWAAATWT
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1025)
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1. .1025
/organism="brosophila melanogaster"
/plasmid="pBeloBAC11"
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/clone_lib="prosBAC"
/clone="bACN11L11"
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- Web: www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Eccal Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Eccal Genetics strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                               LUNSUDED,

DIOSOPHILA melanogaster genome survey sequence TET3 end of BAC:
BACR29P01 of RPCI-9B library from Drosophila melanogaster (fruit
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/db_xref="taxon:7227"
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                                                                                                                       fly), genomic survey sequence. AL069440
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/clone="BACR29P01"
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This GSS 18 part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces tluyveri, Kluyveromyces thermotolerans, Kluyveromyces and lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS 17-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNSO6KHQ 1169 bp DNA linear GSS 17-JUN-200 T3 end of clone ATOAA005D05 of library ATOAA from strain CBS 4311 of Saccharomyces servazzii, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

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FEBS Lett. 487 (1), 3-12 (2000)
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                                       atatttcatatccaagtagatttgataagcaaattcgttttatggaggaaaattcattgg 340
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424 TTATRTAKKTTAAAAAAAAGTGTKWTRATKKKTGKTGDKAARAAADAAATTAAAAAAAA 365
                                                                                                                atttctcagcaactctaatagaattgatagaccaaaaaggaaatttagtatataaaacaac 400
                                                                                                                                                  521 gagatttagtacctgttgaagattatgattttgcaataagaggagctctggctgatttca 580
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                                                                                                                                                                                                                                                                   461 tacttgcccacccaacgtggtgcgtaaaaaagaaagttttcgataagttaatgggatata
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FEBS Lett. 487 (1), 47-51 (2000)
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BM358135 945 bp mRNA linear EST 09-JAN-2002 GA_Ea0005115r Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0005115r, mRNA sequence.
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Sukaryora, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 t 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers
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19,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry, Wood,T.C., Leslie,A. and Wilkins,T.A.
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                                                                                                                                                 /organism="Saccharomyces servazzii"
/strain="CBS 4311"
/db_xref="taxon:27293"
/clone="ATOAA005D05"
/clone_lib="ATOAA05A05"
/note="end : T3"
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 of the genetics, development, and evolution
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/clone="GA_Ea0005115r"
/clone=11b="GGSSypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
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                                      Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4298
Fmax: 864 656 4298
Fmax: 864 656 4298
Fmax: 864 656 4298
Fmay: rwing@clemson.edu
Total High Quality bases = 126
Seq primer: TAATACGACTACTAGGG
High quality sequence start: 3
High quality sequence start: 3
High quality sequence stop: 842.
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/organism="Gossypium arboreum"
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An integrated analysis
of the cotton fiber
Unpublished (2000)
                                                                                                                                                                                                                                                    /strain="AKA'
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illarity 46.1%;
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UNSUZUK7 1092 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 222L11 of library G from Tetraodon nigroviridis, genomic survey sequence.
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.ons.fr/Tetraodon.

Location/Qualifiers
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1 (bases 1 to 1092)

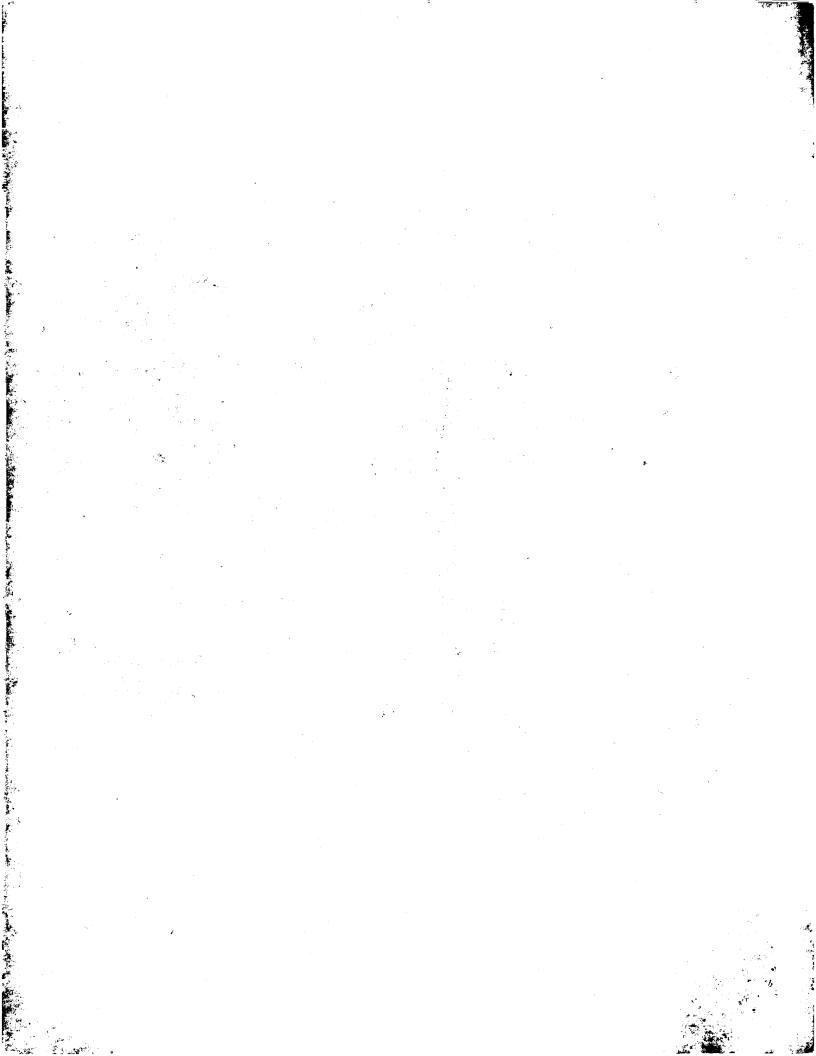
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Bost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J.

Meissenbach, J.

Charleteriation and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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cost-Crollius, H., Jaillon, O., Dasilva, G., Bouneau, L., Fish
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
759 acgctatactcagcaagagctctctaaatattttgagctaaaatctaccctagtattac
                                819 tattagaaaactatatatttgtttatatttatactttaagtctcccttggttaggaggtt
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Tetraodon nigroviridis.
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/note="Genoscope se
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Search completed: August 2, 2002, 12:56:53 Job time: 8219 sec



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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human immune syste	Human immune syste	E. coli 0157 antiq	Escherichia coli f	Enterococcus faeca	Campylobacter jeju	LPS core biosynthe	Human immune syste	Campylobacter jeju
ID	ABL34155	ABL34294	AAX06749	AA256386	AAX13062	AAA53723	AAA53720	ABL33013	AAA53728
DB	24	24	20	21	20	21	21	24	21
% Query Match Length DB ID	15548	5371	14024	14024	4915	906	11474		
% Ouery Match	7.5	7.3	7.3	7.3	7.1	6.9	6.9	6.8	6.8
Score	70.2	9.89	68.2	68.2	67	64.8	64.8	64	63.8
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(EPIG-) EPIGENOMICS AG

LPS core biosynthe	Enterococcus faeca	Chemically pretrea	Tumour suppressor	Campylobacter jeju	Tumour suppressor	Human immune syste	Human inflammatory	Tumour suppressor	Tumour suppressor	Enterococcus faeca	Enterococcus faeca		Streptococcus pneu	e o	Human gene regulat	Human novel protei	Nucleotide sequenc	Chemically pretrea	Tumour suppressor	DNA encoding enzym	Nucleotide sequenc		Plasmodium var-7 p	subunit of	Human immune syste	Human immune syste	2	var-7	Plasmodium var-7 p	Human gene regulat	Human inflammatory			Human immune syste	Human immune syste	
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ALIGNMENTS

Human; immune system disease; cytosine methylation; antiasthmatic; antianaemic; oytostatic; nootropic; antianaemic; oytostatic; nootropic; neuroprotective; anti-HV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclarosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; Human immune system associated gene SEQ ID NO: 2128. BP. ABL34155 standard; DNA; 15548 30-JUN-2000; 2000DE-1032529. 01-SEP-2000; 2000DE-1043826. 02-JUL-2001; 2001WO-EP07537. (first entry) 40200200928-A2. Homo sapiens 26-MAR-2002 03-JAN-2002 ABL34155; ABL34155/c ID ABL341 dene; ~

Fri Aug

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gene; ds.
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                                                                                                               The present invention provides a number of human immune system associated dense which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11480 ATATATTCCATTACATTATTCTTTACAAACATTCATTTAATTATATAATTACTAATTAAT 11421
                                                                                                                                                                                                                                                                                                                        12140 ATATATAACATATAAAATAACATATAAAAATAACATATAAAAATAACATATAAAAATAA 12081
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                                                                                                                                                                                                                                                                             Gaps
                                             leic acid comprising fragment of chemically modified gene, useful diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                cggtgaaaatttctaagggagaatatattttagaatggatgctgatgtatttcatatc
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                                                                                                                                                                                                                                                     Length 15548;
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                                                                                                                                                                                                                    Sequence 15548 BP; 4209 A; 247 C; 2903 G; 8189 T; 0 other;
                                                                                          Claim 1; SEQ ID NO 2128; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                    Score 70.2; DB 24;
Pred. No. 0.00037;
0; Mismatches 413;
Berlin K;
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                                                                                                                                                                                                                                                    7.5%;
ilarity 44.3%;
Conservative
 Piepenbrock C,
                                              Nucleic acid comprising
                                                                     cytosine methylation
                      WPI; 2002-130909/17
                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                          Matches 332;
                                                                                                                                                                                                                                                      Query Match
 Olek A,
                                                                                                                                                                                                                                                                  Local
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alls, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antinflammatory; cancer disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO: 2267.
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0; Mismatches 264;
                                          11420 TACTTAATTATTATAACAACGAAATATT 11392
889 gatattaatattttagtactgaaattgtt
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01-SEP-2000; 2000DE-1043826
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Matches 239; Conserv
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                                                                                                                                                                                                                                                                                                                        Wang L;
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Best Local Similarity
                                                                                                                                    repeat_region
         AAW88317" CDS
                                                                                                                                                                                                                                                                               22-JUL-1997;
01-MAY-1997;
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 1447
                                        1624 TACATAAAACCCTCATAACAAACCAAAACAAATTATCAAATATAACAAATCCAACCTTA 1565
                                                                         1564 AATAAAATCATTCATACGTATAAATAATAAACTTTTAAACTTAAACGCACCCAACTCAAT 1505
                                                                                                                                          ataagtttaagcaatatatttactcagctattttacaagattttataaagaaaaatctt 706
                                                                                                                                                                                                                                                                                                                     O antigen; O157 antigen; diagnosis; wbdN gene; wzx gene; wzy gene; wbdP gene; wbdO gene; wbdR gene; transferase; polymerase; flippase; diarrhoea; haemorrhagic colitis; ds.
                                                                                                 gtaataaaatatacttaactaatgatatacggaagatgttattgaatagatctatacttg
                                                        467 cccacccaacgtggtgcgtaaaaaaagaaagttttcgataagttaatgggatatagagatt
                                                                                          tagtacctgttgaagattatgattttgcaataagaggagctctggctgatttcaaaatcg
                                                                                                                         587 gcttactcaataaagtacttttacagtatagattaaacgagaatggaatatcacaaacca
                                                                                                                                                                                                                                                                                                                                                                                                /product= sugar_transferase
/note= "wbdN gene (ORF1), this region is
    specifically claimed in Claim 6; encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                          encodes
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product= perosamine_synthetase
/note= "per gene (ORF5); encodes AAW88316"
5257..6471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= d
/product= O_antigen_flippase
/note= "wzx gene (ORF4), this region is
specifically claimed in Claim 6; v
4132..5232
                                                                                                                                                                                                                                                                                                                                                                                                                                        L* O_antigen-polymerase
"way gene (ORP2), this region is
specifically claimed in Claim 6;
2011..2757
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6;
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/note- "wbdP gene (ORF6), this region is
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/note= "wbdo gene (ORF3), this region
specifically claimed in Claim
2744..4135
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
79..861
                                                                                                                                                                                                                                                                                                                                                                                                                         858..2042
                                                                                                                                                                                                          1326 ATTAAAATATCTATATAAATATAAA 1302
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                                                                                                                                                                                                                                                                                                     E. coli 0157 antigen gene cluster.
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/note= "wzy
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P-PSDB; AAW88312, AAW88313, AAW88314, AAW88315, AAW88316, AAW88317,
AAW88318, AAW88319, AAW88320, AAW88321, AAW88322, AAW88323.
                                                                                                                                                                                                                                                                                                            may play a role in gene cluster
                                                                                                                                                                                                                                                                                                                                                                                              /note= "wbdR gene (ORF12), this region is specifically claimed in Claim 6; encodes AAW88323"
 6; encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food, faeces or patient samples
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                                                                                                                                                                                                    /note= "manC gene (ORF10); encodes AAW88321"
[0523..11893
                                                                                                                                                                                                                                                      /note= "manD gene (ORF11); encodes AAW88322"
12007..13123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14024 BP; 4546 A; 2263 C; 2832 G; 4383 T; 0 other;
specifically claimed in Claim 6491..7609
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Pred. No. 0.00084;
                                g
"ORF7; encodes AAW88318"
                                                                                                                                                'note= "ORF9; encodes AAW88320"
                                                                                                    encodes AAW88319"
                                                                                                                                                                                                                                                                                                                                                                            /product- N-acetyl_transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cause diarrhoea and haemorrhagic colitis.
                                                                                                                                                                                                                                                                                                 'note= "H-repeat,
                                                                                                                                                                                                                                                                                                                              assembly
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52.5%;
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97AU-0006545.
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                                                /note= "ORF
7606..8578
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8580..9089
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Enterococcus faecalis
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16-MAY-1997;
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                               273
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                                                                                                                                                                                                                   393
                                                                ttaaatcaaacgettaettgattttgagtteataattgteattgataatecaagtagaggt 132
                                                                                                         gatttaaagcaattettaacagaatatteagttgtagataatagaataaaaatettgett 192
                                                                                                                                                    aatgaagaaaatattggtttagcatcaagtttgaacaaagcggtgaaaatttctaaggga 252
                                                                                                                                                                                                                                         attogitittaiggaggaaaattoattggaittoicagoaactotaatagaattgatagac 372
                                                                                                                                                                                                                                                             394 atcgaagtgttaaataatgaatgtgtagatgtgtagtatgttctaattattattatagat 453
                    atcattatgtcggtatataatgagcctttaaattatgtgagagattcagtagaatctata 72
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli flagellin protein nucleotide sequence SEQ ID NO:56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid molecule useful for the detection of flagellated
                                                                                                                      157 atacatcaatcttatcaagattttg---ttttgtatatcattgacgattgtagcaccgat
                                                                                                                                                                gaatatatttttagaatggatgctgatgatatttcatatccaagtagatttgataagcaa
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9
  Indels
 Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Flagellin; fliC; antigen; detection; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 229-233; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                            AAZ56386 standard; DNA; 14024 BP.
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                                                                                                                                                                                                                                                                                 373 caaaaaggaaatttagt 389
| | | | | | || | | | |
454 aacaatagaaatattgt 470
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1998;
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198;
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serotype in the sample. (I) are useful for: (1) detecting the presence of E. coli of H serotype in a sample by hybridising at least one or a pair of (I) to any E. Coll in the sample and detecting the hybridised nucleic acid molecules; and (2) for detecting the presence of both O and H-serotypes of E. coli by hybridising at least one or a pair of (I) to any E. coli present in the sample and detecting the hybridised nucleic acid molecules. (I) is particularly useful for detecting the Combination of O and H antigen. Hybridised (I) when using at least one (I) is detected by southern blot analysis and, when using a pair of (I), is detected by polymerase chain reaction (PCR). AAZ56399 to AAZ56420 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 atacatcaatcttatcaagattttg---ttttgtatatcattgacgattgtagcaccgat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 14024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14024 BP; 4546 A; 2263 C; 2832 G; 4383 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.3%; Score 68.2; DB 21;
Best Local Similarity 52.5%; Pred. No. 0.00084;
Matches 198; Conservative 0; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX12038 to AAX1319 represent these nucleotide sequences is against the sequences is also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for progression of disease, and for identifying agents which can be used for modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || | | ||||||| || ||||| || ||||| || ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      computer readable medium has been developed which has recorded on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4045 AAAAAGATTCAAGAATCTTTTTACTGAAAAATGAACAGAACATGGCATTGCAAAGACCA 3986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                          New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biosynthetic locus; biosynthesis; lipid A biosynthesis; acetyltransferase; acetyltransferase; alycosyltransferase; Beta-1, 4-galactosyltransferase; alpha-2,3-sialyltransferase; sialic acid synthase; CMP-sialic acid synthetase; mimic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campylobacter jejuni OH4384 Beta-1,3-galactosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4915 BP; 1465 A; 950 C; 750 G; 1740 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 759-761; 2084pp; English.
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                                                                       Kunsch CA;
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(HUMA-) HUMAN GENOME SCI INC.
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                                                                   Dillon PJ,
                                                                                                                                       WPI; 1999-045171/04
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                                                                   Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nfection
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A reaction mixture for the synthesis of a sialylated oligosaccharide is useful for synthesising sialylated oligosaccharide such as another single, lysoganglioside or their minics. Glycosyltransferases are useful for chemo-enzymatic synthesis of oligosaccharides, including gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside minics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside minetic synthesis. Antibodies raised against the glycosyltransferases are also useful for analyzing the expression patterns of these genes involved in pathogenesis. The oligonucleotides for inhibiting expression of the Campylobacter oligonucleotides for inhibiting expression of the Campylobacter enzymes that are involved in the biosynthesis of ganglioside minics that can mask the pathogens from the host's immune system. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel glycosyltransferase polypeptides and polynucleotides useful for blosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
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Pred. No. 0.0032;
); Mismatches 157; Indels 3.
                                                                            /*tag= a
/product= Beta-1,4-galactosyltransferase
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Location/Qualifiers
1..906
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31-JAN-2000; 2000US-0495406.
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Best Local Simi
Matches 172;
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5842 TGTGGAAATGATAATAGTATAAATATAGCCAAAGAATACTCTAAAAAAAGACAAAAGAATA 5783
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                                                                                                            Gilbert M,
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181 aaaatcttgcttaatgaagaaaatattggtttagcatcaagtttgaacaaagcggtgaaa 240
                                        241 atttctaagggagaatatattttagaatggatgctgatgatatttcatatccaagtaga 300
                                                                                                                                                                                                                          Blosynthetic locus; biosynthesis; lipid A biosynthesis; acetyltransferase; Beta-1,4-GallMc transferase; Beta-1,3-galactosyltransferase; alpha-2,3-sialyltransferase; sialic acid synthase; CMP-sialic acid synthetase; mimic; antibody; immunogen; ganglioside; ds.
                                                  178 aaaataatccacaatgaaaaaaacttaggtcttttaagagcaagatatgaaggtgtgaaa
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note= "Open reading frame 6a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product = Sialic acid biosynthetic enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= CMP-sialic acid synthetase
/note= "Open reading frame 10a"
complement (10554..11366)
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/note= "Open reading frame 3a"
?786..3955
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1234..2490
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5054..5959
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1924..7964
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                                                                              301 tttgataagcaaattcgttttatggaggaaaa 332
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                                                                                                                                                                                                                                                                                                                                       'product= acyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A reaction mixture for the synthesis of a sialylated oligosaccharide is useful for synthesising sialylated oligosaccharide such as ganglioside, lysoganglioside or their mimics. Glycosyltransferases are useful for chemo-enzymatic synthesis of oligosaccharides, including gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimetic synthesis. Antibodies raised against the glycosyltransferases are also useful for analyzing the expression patterns of these genes involved in pathogenesis. The nucleic acids are also useful for designing antisense.
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AAX97206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel glycosyltransferase polypeptides and polynucleotides useful biosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
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Pred. No. 0.0034;
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51.8%;
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31-JAN-2000; 2000US-0495406.
01-FEB-2000; 2000WO-CA00086
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Matches 172; Conservative
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22-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reluxenia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/vlocrative bowel diseases. The present sequence is a gene of the invention.
acaaagcggtgaaaatttctaagggagaatatattttagaatggatgctgatgatattt 286
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                                                                                                                                                                                                          Human; immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, use for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7597 BP; 1965 A; 109 C; 1790 G; 3733 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 375; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 986; 32pp + Sequence Listing; German
                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64; DB 24;
Pred. No. 0.0048;
                                                       5662 TGTGAAGAGTGTATAAAATTTTAGATGAACA 5631
                                 tttgataagcaaattcgttttatggaggaaaa 332
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                                                                                                               ABL33013 standard; DNA; 7597
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                             (first entry)
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Best Local Similarity 45.2'
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                                                                                                                                                           26-MAR-2002
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                                                                                                                                      ABL33013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           706 tatattgatatcacaaaaattactaattactttcaagagtatgtgataaagaaacgctat
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                                                       tcagcaactctaatagaattgatagaccaaaaaggaaatttagtatataaacaacgagaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 CGAATAAATACATAAATAAATAAA 178
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31-JAN-2000; 2000US-0495406.
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                                                                                                                                                                               A reaction maximite for the synthesis of a starytated origosaccharide ganglioside, lysoganglioside or their mimics. Glycosyltransferases are useful for synthesising sialylated oligosaccharides, are useful for chamo-enzymatic synthesis of oligosaccharides.

Including gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside mimics, such as C. jojuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimics, such as C. jojuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimics. Antibodies raised against the glycosyltransferases are also useful for designing antisense oligonucleotides for inhibiting expression of the Campylobacter enzymes that are involved in the biosynthesis of ganglioside mimics that can mask the pathogens from the host's immune system. The oligosaccharides are useful as dlagnosing reagents or as therapeutics and as immunogens for producing antibodies. Bacterial glycosyltransferase can be used to catalyse the formation of structures and are easier and less expensive to produce in large quantity. Compared to the mammalian glycosyltransferase. The bacterial origin of the enzymes facilitates expression of large cannellias of the enzymes facilitates expression of large cannellias systems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaattatgtgagagattcagtagaatctatattaaatcaaacgcttactgattttgagtt 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                       reaction mixture for the synthesis of a sialylated oligosaccharide
                                                                                              Novel glycosyltransferase polypeptides and polynucleotides useful biosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 agttgtagataatagaataaaaatcttgcttaatgaagaaaatattggtttagcatcaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 63.8; DB 21; Length 1170;
Pred. No. 0.0049;
0; Mismatches 102; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1170 BP; 504 A; 120 C; 171 G; 375 T; 0 other;
                                                                                                                                               Disclosure; Page 99; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA53720 standard; DNA; 11474 BP.
         (CANA ) NAT RES COUNCIL CANADA.
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                                   Wakarchuk WW;
                                                         WPI; 2000-524418/47.
P-PSDB; AAY97202.
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                                  Gilbert M,
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Best Local S
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Novel glycosyltransferase polypeptides and polynucleotides useful for
                                         Biosynthetic locus; biosynthesis; lipid A biosynthesis; acetyltransferase; Beta-1,4-GalNAc transferase; Beta-1,3-galactosyltransferase; alpha-2,3-sialyltransferase; seta-1,2-galactosyltransferase; alpha-2,3-sialyltransferase; sialic acid synthesis; CMP-sialic acid synthetase; mimic; antibody; immunogen; ganglioside; ds.
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P-PSDB; AAY97200, AAY97201, AAY97202, AAY97203, AAY97204, AAY97205,
AAY97206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product Lipooligosaccharide biosynthetic enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= Sialic acid biosynthetic enzyme/note= "Open reading frame 9a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= Beta 1,2- galactosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product= Beta 1,4-GalNAc transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= CMP-sialic acid synthetase
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/product= Sialic acid synthase
/note= "Open reading frame 8a"
8020..9079
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/product= Glycosyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                       transferase
                                                                                                                                                                                                                                                                                                                                  "Open reading frame 2b"
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6048..6923
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                                                                                                                                                                                                                                                                                                          'product= acyltransferase
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                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     /product= glycosyl
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31-JAN-2000; 2000US-0495406.
                                                                                                                                                                                      Campylobacter jejuni OH4384.
LPS core biosynthesis locus
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6924..7964
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5054..5959
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9076..9741
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                                                                                          A reaction mixture for the synthesis of a slalylated oligosaccharide is useful for synthesising slalylated oligosaccharide such as ganglioside, lysoganglioside or their mmines. Glycosyltransferases are useful for chemo-enzymatic synthesis of oligosaccharides, concluding gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimmeric synthesis. Antibodies raised against the glycosyltransferases are also useful for analyzing the expression patterns of these genes involved in pathogenesis. The oligonucleotides for inhibiting expression of the Campylobacter enzymes that are involved in the biosynthesis of ganglioside mimics that can mask the pathogens from the host's immune system. The oligosaccharides are useful as diagnosing reagents or as therapeutics and as immunogens for producing antibodies. Bacterial and as immunogens for producing antibodies. Bacterial oligosaccharides that are identical to the corresponding mammalian structures and are easier and less expensive to produce in large quantility, compared to the mammalian glycosyltransferase. The mammalian glycosyltransferase in large quantility compared to the mammalian glycosyltransferase.
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blosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
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vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 11474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11474 BP; 4506 A; 1495 C; 1613 G; 3860 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63.8; DB 21; Length
Pred. No. 0.0052;
0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  faecalis genome contig SEQ ID NO:201.
                                                          Claim 1; Page 86-90; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX13138 standard; DNA; 5154 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 56.8
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression systems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus
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Enterococcus faecalis

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982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                     recorded on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1517 ACAAAATCAGTACTATGAAAATTGGGAGTTATGTTTAGCAGATGATGCATCGCCAAGCGA 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1457 ACATATTAAGCCAATGCTAGAAAATATAAAGAACTAGATCAACGAATCAAAGTTATTTA 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1397 TCGCGAAGAAAACGGACATATTTCAGAAGCAACTAACTCAGCTTTGTCGATTGCTACTGG 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgatttaaaagcaattcttaacagaatattcagttgtagataatagaataaaaatcttgct 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 attaaaatcaaacgettactgattttgagttcataattgtcattgataatccaagtagagg 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                        New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 tatcattatgtcggtatataaatgagcctttaaattatgtgagagattcagtagaatctat 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     computer readable medium has been developed which has
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                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1062-1065; 2084pp; English.
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                                                                                                                                                                                                                                     Kunsch
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                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                       98WO-US08985
                                                                                                                         6009900-sn26
                                                                                                                                            97US-0044031
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                                                                                                                                                                                                                                 Dillon PJ,
                                                                                                                                                                                                                                                                     WPI; 1999-045171/04.
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               W09850555-A2
                                                                                                                         14-NOV-1997;
                                                                                       04-MAY-1998;
                                                                                                                                            06-MAY-1997;
                                                                                                                                                           16-MAY-1997;
                                                   12-NOV-1998
                                                                                                                                                                                                                                 Barash SC,
                                                                                                                                                                                                                                                                                                                                                                 infection
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Sequences AAS45296-AAS4550 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinuclectides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis,
                                                                     Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 tttaaaagcaattcttaacagaatattcagttgtagataatagaataaaaatcttgcttaa 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle -
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                                  pretreated genomic DNA associated with cell cycle #45.
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44.3%; Pred. No. 0.0072;
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0; Mismatches 458;
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
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(first entry)
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                                                                                                                                                                                                       Homo sapiens.
18-DEC-2001
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                                  Chemically
                                                                                                                                                                   PCR primer
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Matches
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1491 ATTTATCTCACGAA----TAATATAAAAAAAAAAATAATTCACAATAAAAAAATAATC 1436
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                                                                                 aaaaggaaatttagtatataaacaacgagaaagtaataaaattacttaactaatgatat 434
                                                                                                                                  agttttcgataagttaatgggatatagagatttagtacctgttgaagattatgattttgc
                                                                                                                                                                                                          aataagaggagctctggctg-atttcaaaatcggcttactcaataaagtacttttacagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour suppressor gene; oncogene; antitumour; cytostatic; tumour; CpG dinucleotide; single-nucleotide polymorphism;
                                                                                                           atagattaaaacgagaatggaatatcacaaaccaataaagtttaagcaatatatttactcag
                                                                                                                                                                                                                                                                                                                                 ctattttacaagatttttataaagaaaatcttatattgatatcacaaaaattactaatt
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                                                                                                                                                                                                                                                                                                                                                                                                                               794 agctaaaaatctacccctagtattactattagaaaactatatatttgtttatatttatact
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20000E-1019173.
20000E-1032529.
20000E-1043826.
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cytosine methylation; ds.
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07-APR-2000;
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(EPIG-) EPIGENOMICS AG.

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255 atatatttttagaatggatgctgatgatatttcatatccaagtagatttgataagcaaat 314

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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genea associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an erray for analysing diseases associated with Cpc dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or thrapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters. The parameters of the compared to another set of genetic and/or prognosis events which are bisate and any present sequence is one of the formatic parameters and the problem of the finance and the proper and sequence and sequence are disadvantageous to patients. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
                                                                                                             tumour suppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                        of chemically modified genes associated with tumour supponcogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 genomic sequences derived from tumour suppressor genes and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.7%; Score 63; DB 22; Length 5689;
14.3%; Pred. No. 0.0072;
ve 0; Mismatches 458; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                     Claim 1; SEQ ID No 148; 27pp; English
                    Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this
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                    Plepenbrock
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                                                                                                        Fragments
genes and
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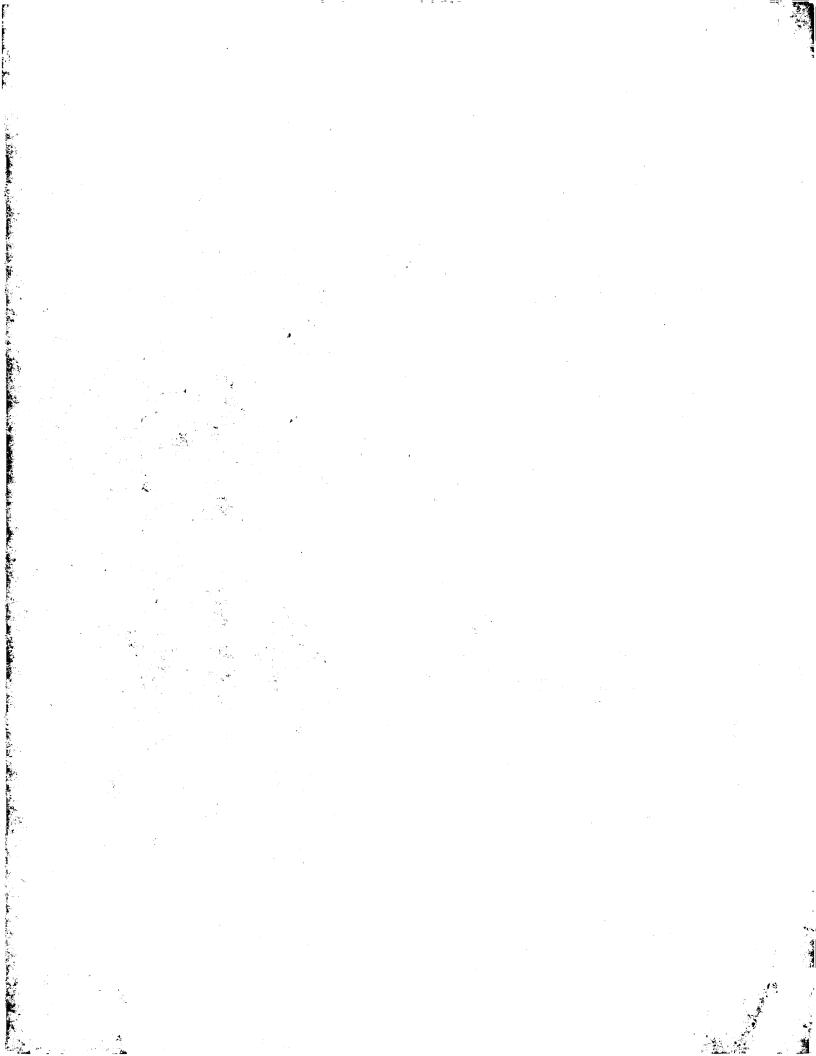
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ACGTTAAAAATATATATATATATAAAAAAAAAAACACCTACGATACACAAATCGTATACA 1492
                                                                                                                                  Novel glycosyltransferase polypeptides and polynucleotides useful for
 agttttcgataagttaatgggatatagagatttagtacctgttgaagattatgattttgc 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biosynthetic locus; biosynthesis; lipid A biosynthesis; cecyltransferase; Beta-1, 4GalNMc transferas, Beta-1, 3-galactosyltransferase; alpha-2, 3-sialyltransferase; sialic acid synthase; CMP-sialic acid synthetase; mimic; antibody;
                                                     aataagaggagetetggetg-attteaaaateggettaeteaataaagtaettttaeagt
                                                                                                        atagattaaacgagaatggaatatcacaaaccaataagtttaagcaatatatttactcag
                                                                                                                                                            ctattttacaagatttttataaagaaaaatcttatattgatatcacaaaaattactaatt
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                                                                                                                                                                                                                                                                                             1315 TAATITAATATAATTAAAAATAAAAATAACA-TATATICATCTATACAATICATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
                                                                                                                                                                                                                 actttcaagagtatgtgataaagaaacgctatactcagcaagagctctctaaatattttg
                                                                                                                                                                                                                                                                                                                                       854 ttaagtctcccttggttaggaggttattaataaaatgatattaatattttagta 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campylobacter jejuni beta-1,3-galactosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunity; immunogen; ganglioside;
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAA53727 standard; DNA; 912 BP
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31-JAN-2000; 2000US-0495406.
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                                                           is useful for synthesising slatylated oligosaccharides such as are useful for synthesising slatylated oligosaccharides such as are useful for chemo-enzymatic synthesis of oligosaccharides, including gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimetic synthesis. Antibodies raised against the glycosyltransferases are also useful for analyzing the expression patterns of these genes involved in pathogenesis. The oligonuclebrides for inhibiting expression of the campylobacter oligonuclebrides for inhibiting expression of the campylobacter cards are also useful for designing antisense oligonuclebrides for inhibiting expression of the campylobacter cards are involved in the biosynthesis of ganglioside mimics that can mask the pathogens from the host's immune system. The
                                                                                                                                                                                                                                                                                                                   oligosaccharides are useful as diagnosing reagents or as therapeutics and as immunogens for producing antibodies. Bacterial glycosyltransferase can be used to catalyse the formation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 atttctaagggagaatatattttagaatggatgctgatgatatttcatatccaagtaga 300
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                                                A reaction mixture for the synthesis of a sialylated oligosaccharide
                                                                                                                                                                                                                                                                                                                                                       oligosaccharides that are identical to the corresponding mammalian structures and are easier and less expensive to produce in large quantity, compared to the mammalian glycosyltransferase. The bacterial origin of the enzymes facilitates expression of large quantities of the enzymes using relatively inexpensive prokaryotic expression systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human: tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 atgagtcaaatttccatcatactaccaacttataatgtggaaaaatatattgctagagca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 aaaatcatacataatgaagagaatttaaagcttttaagagcaagatatgaaggtgctaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ccaagtagaggtgatttaaagcaattcttaacagaatattcagttgtagataatagaata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.4%; Score 60.4; DB 21; Length 912;
31.2%; Pred. No. 0.02;
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0; Mismatches 156;
               Disclosure; Page 103; 120pp; English
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Best Local Similarity 51.2'
Matches 167; Conservative
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretracted DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and concepenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences complementary to (53). The nucleic acid may be a peptide nucleic acid most peptide nucleic acid probes for detecting the cytosine methylation state and/or single nucleide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fragments of chemically modified genes associated with tumour suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 aactctaatagaattgatagaccaaaaaggaaatttagtatataaaacaacgagaaagtaa 410
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46.6%; Pred. No. 0.021;
live 0; Mismatches 221;
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                                                                                                                                                                                                                                                                                                                                    06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1048826.
                                                                                                                                                                                                                         15-MAR-2001; 2001WO-EP02955
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                                                                       WO200168912-A2.
Homo sapiens.
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Search completed: August 2, 2002, 13:32:33 Job time: 4229 sec



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us-09-900-038a-2.rni

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:
August 2, 2002, 10:47:14; Search time 49.3 Seconds
(without alignments)
4678.496 Million cell updates/sec
1 atgantatagtatcattat......gaggagagaaacaaagtgac 939
Sequence:
1 atgantatagtatcattat......gaggagagaaacaaagtgac 939
Scoring table:
Gapop 10.0, Gapext 1.0
Searched:
383533 seqs, 122816752 residues
Total number of hits satisfying chosen parameters:
767066
Manimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Issued_Patents_NA:*
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2: /cgn2_c/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_c/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_c/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_c/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_c/ptodata/2/ina/PcTUS_COMB.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SUMMARIES

		ф			SUMMAKIES	
Score	41	Query	Query Match Length DB	ВО	ID	Description
56.6	l o	6.0	19124	7	US-08-487-826B-13	Sequence 13, Appl
55.6	9	5.9	19124	7	US-08-487-826B-13	Sequence 13, Appl
•	ij	5.4	854	4	US-08-998-416-534	534,
	20	5.3	860	4	US-08-998-416-287	287,
	ဂ္က	5.3	6124	❖	US-08-213-419B-3	3, A
49	7.	5.3	7218	-	US-08-232-463-14	14
48	ω.	5.2	1882	Н	US-08-257-073-12	12,
48.8	Φ.		1884	-	US-08-257-073-8	. , 8
48	φ.	5.5	615	4	US-08-998-416-186	186
47	9		844	m	US-08-961-083-195	195,
47	4.	5.0	837	4	US-08-998-416-288	288,
	46	4.9	3701	4	US-08-845-258-10	
•	9	4.9	3701	4	US-08-990-571-10	10,
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45.	9	4.9	6152	4	US-08-973-462-1	1, 1
45	ø	4.9	8920	~	US-08-446-855A-1	1,
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45	٧.	4.8	658	4	US-08-998-416-595	59
44	4.	4.7	837	4	US-08-998-416-288	288,
44	Ŋ	4.7	732	4	US-08-998-416-1036	Sequence 1036, Ap
	44	4.7	724	4	US-08-998-416-683	683,
43	Ф.	4.7	688	4	US-08-998-416-972	972,
43	3.8	4.7	1664	4	US-08-936-165A-259	
43	₹.	4.6	782	4	US-08-998-416-224	Sequence 224, App
•	2	4.6	167	4	US-08-998-416-472	472,

6.0%; Score 56.6; DB 2; Length 19124;

Query Match

Sequence 191, App Sequence 191, App Sequence 191, Appl Sequence 32, Appl Sequence 4, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 1092, Ap Sequence 244, App Sequence 241, App Sequence 541, App Sequence 541, App Sequence 541, App Sequence 541, App Sequence 541, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl		THROCYTE BINDING PROTEINS
US-08-998-416-191 US-08-998-416-191 US-08-617-8608-32 US-08-617-8608-32 US-08-920-812-6 US-08-920-812-6 US-08-921-177-6 US-08-921-177-6 US-08-998-416-1092 US-08-998-416-24 US-08-998-416-24 US-08-998-416-534 US-08-998-416-534 US-08-998-416-534 US-08-998-416-534 US-08-998-416-534 US-08-998-416-534 US-08-998-416-534 US-08-998-416-534 US-08-998-416-87	ALIGNMENTS	ication US/08487826B 7 10N: m, Kim L. itnis, Chetan iller, Louis H. terson, David S. Xin-zhaun TION: BINDING DOMAINS FROM PLASMODIUM VIVAX TION: AND PLASMODIUM FALCIPARUM ERTHROCYTE ENCES: 45 ENCES:
663 663 663 663 663 663 663 663 663 663		GULT 1 08-487-826B-13/C Gequence 13, Application US/08487826B Catent No. 593827 GENERAL INFORMATION: APPLICANT: Sim, Kim L. APPLICANT: Application David S. APPLICANT: Miller, Louis H. APPLICANT: Miller, Louis H. APPLICANT: Miller, Louis H. APPLICANT: Su, Xin-zhaun APPLICANT: Wellems, Thomas E. TITLE OF INVENTION: AND PLASMODIUM CONNERS OF SEQUENCES: 45 CONNERS OF SEQUENCES: ADDRESS: 810, COMPUTER: EADDABLE FORM: MEDIUM TYPE: PATENTIN RC-DOS/MS-DOS SOFTWARE: BATE 10, SEP-1993 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN RC-SEP-1993 CLASSIFCATION NUMBER: US/08/487, 82 TILING DATE: 10, SEP-1993 CLASSIFCATION NUMBER: US/08/487, 82 TELEPHONE: (619) 235-0176 INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 19124 base pairs TYPE: nucleic acid STRANDEDNESS: Single TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO ORANTI-SENSE: NO ORANTI-
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		13, Appl 13, Appl 13, Appl ANT: Si ANT: Ch ANT: Ch ANT: Ch ANT: Ch ANT: We OF INVEN OF INVEN TANT: We ADDENCE IET: Cali TYPE: Cali
0 000000 00000000000000000000000000000		RESULT 1 US-08-487-8 Sequence Sequence Patent N APPLIC APP
		

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FILING DATE: 10-SEP-1993
CLÁSSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REGISTRATION NUMBER: NIH12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-8550
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ANTI-SENSE:
US-08-487-826B-13
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                                                       gtatcattatgtcggtatataatgagcctttaaattatgtgagagattcagtagaatcta 70
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 0.00073;
   Pred. No.
43.68;
                 Conservative
 Similarity
Best Local
Matches 36
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: 19124 base pairs nucleic acid

LENGTH:

TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear

MOLECULE TYPE: HYPOTHETICAL: 1

SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/487,826B FILING DATE: IO-SEP-1993 CLASSIFICATION: 435

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

92660

COUNTRY:

CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor

OF SEQUENCES:

CITY: Newport Beach STATE: California

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334 tcattggatttctcagcaactctaatagaattgatagaccaaaaaggaaatttagtatat 393
                                                          tttgagttcataattgtcattgataatccaagtagaggtgatttaaaggcaattcttaaca 153
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Score 55.6; DB 2;
Pred. No. 0.0012;
Query Match 5.9%;
Best Local Similarity 42.5%;
Matches 351; Conservative
                                                          94
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Sequence 13, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitchis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

US-08-487-826B-13

1;

Length 19124;

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PAG1372UP
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; ORGANISM:
US-08-998-416-534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                101
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                                                                                                                                16097 ATATATATATATATACCCATAACTACATACATATACATTAACAAACACATATATAA 16156
                                                                                                             694 aaagaaaaat cttatattgatatcacaaaaattactaattacttcaagagtatgtgat 752
                                                 atatcacaaaccaataagtttaagcaatatatttactcagctattttacaagatttttat
                                                                                                                                                                               753 aaagaaacgetatacteageaagagetetetaaatattttgagetaaaatetaeeeetag
                                                                                                                                                                                                                                                813 tattactattagaaaactatatatttgtttatattttatactttaagtctcccttggttag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Philippsen, Peter
APPLICANT: Poblmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      873 gaggttattaataaatgatattaatattttagtactgaaattgttt 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION 435
PRIOR APPLICATION A 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REPERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELETOMES 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 534, Application US/08998416
Patent No. 6229264
GENEAL INFORMATION:
APPLICANT: Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 854 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
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161 cagttgtagataatagaataaaaatcttgcttaatgaagaaaatattggtttagcatcaa 220
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                                                                                                                                41 taaattatgtgagagattcagtagaatctatattaaatcaaacgcttactgattttgagt 100
                                                                                                                                                                                         649 TAAAATAAATAGAAACCATAAGTTAATTGATTCATAAAGAAAATGGAATTATTGTGGCA 590
                                                                                                                                                                                                                                                           tcataattgtcattgataatccaagtagaggtgatttaaagcaattcttaacagaatatt 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gatttctcagcaactctaatagaattgatagaccaaaaaggaaatttagtatataaaacaa 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 TTAATTGGATATTACTACCTACTAAATATTTACCTA-ATAATATATTATTAAGAATACTT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 AAATTATTATTAATTAGTAAATTATATTATTATTATTAACATAATTTTTGATAAT 111
                                                                                                                                                                                                                                                                                                  APPLICANT: Philippsen, Peter APPLICANT: Philippsen, Rainer APPLICANT: Pohlmann, Rainer APPLICANT: Steiner, Sabine APPLICANT: Mohr, Christine APPLICANT: Mont, Christine APPLICANT: Mendland, Jurgen APPLICANT: Rectile, Philipp APPLICANT: Rebischung, Corinne TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII TITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
                                                                  5;
   Length 854;
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580 aaaatcggcttactcaataaagtacttttacagtatagattaaacga 626
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Pred. No. 0.0072;
0; Mismatches 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 287, Application US/08998416; Patent No. 6239264; GENERAL INFORMATION: APPLICANT: Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 6239264th Carolina
: USA
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CITY: Research Triangle Park
Query Match 5.4%;
Best Local Similarity 45.1%;
Matches 265; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Inselburg, J. et al.

TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: JII-002CNCP
CURRENT APPLICATION NUMBER: US/08/213,419B
FRICH APPLICATION NUMBER: US 07/870,506
PRIOR FILING DATE: 1992-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 agatttgataagcaaattcgttttatggaggaaaattcattggatttctcagcaactcta 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 atagaattgatagaccaaaaaggaaatttagtatataaacaacgagaaagtaataaaata 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 tacttaactaatgatatacggaagatgttattgaatagatctatacttgcccaccaacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               598 aaagtacttttacagtatagattaaacgagaatggaatatcacaaaaccaataagtttaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.3%; Score 50; DB 4; Length 6124; Best Local Similarity 44.3%; Pred. No. 0.016; Matches 203; Conservative 0; Mismatches 255; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2589 ttttttttaggtgttatatttaacaaaaagttataaa 2626
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                                                            Sequence 3, Application US/08213419B Patent No. 6333406 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO SEQ ID 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | LCCATION: (2407)...(2439)
| NAME/KEY: CDS
| LOCATION: (2598)...(3404)
| NAME/KEY: CDS
| LCCATION: (3580)...(3720)
| NAME/KEY: CDS
| LCCATION: (3850)...(5835)
| US-08-213-419B-3
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                                         US-08-213-419B-3
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 ITAATTAAATCTTTTTTTTTTTTTTTAAATTATTATTAATTAGTAAATTATATTTTT 138
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                               NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFRAX: 919-541-8689
                                                                                      APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 287: SEQUENCE CHARACTERISTICS: LENGTH: 860 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tatagattaaacga 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: PAG1240UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                             FILING DATE: 24 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-998-416-287
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526 TTAAAAGATGGAGGTTTTGCTTTTCCTCCAACAGAACCTCTTATGTCACCAATGACATTA 585
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                                                   483 cgtaaaaaagaaagttttcgataagttaatgggatatagagatttagtacctgttgaag
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                                                                                                                                                                                                          APPLICANT: de Taisne, Charles
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48.8; DB 1;
Pred. No. 0.024;
0; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 20-WAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/075,783
FILIND DATE: 11-010-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
FILIND DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              New York
: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                         Sequence 12, Application US/08257073
Patent No. 5766597
GENERAL INFORMATION:
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TELEFAX: (212) 840-0712
TELEX: 42506 CURMA
INFORMATION FOR SEQ ID NO: 12:
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ilarity 47.4%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UN
                                                                                                                  RESULT 7
US-08-257-073-12
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Matches 146;
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                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.3%; Score 49.4; DB 1; Length 7 Best Local Similarity 9.1%; Pred. No. 0.022; Matches 38; Conservative 200; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.25
                APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY, AGGNT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMM TELECOMMUNICATION INFORMATION: TELECHONE: (703)836-9300
                                                                                                                                    E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                              ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-232-463-14
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GENERAL INFORMATION
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                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                     STREET:
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526 TTAAAAGATGGAGGTTTTGCTTTTCCTCCAACAGAACCTCTTATGTCACCAATGACATTA 585
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                                                                                                                                                                                              346 tcagcaactctaatagaattgatagaccaaaaaggaaatttagtatataaacaacgagaa 405
                                                                                                                                                                                                                                                                                                706 TATCCAGCTGTTTATGATGACAAAGATAAAAGTGTCATATTATTATATTGCAGCTCAA 765
166 gtagataatagaataaaaatcttgcttaatgaagaaaatattggtttagcatcaagtttg
                                                                                226 aacaaagcggtgaaaatttctaagggagaatatattttagaatggatgctgatgatatt
                                                                                                                        586 GATGAAATGAGACATTTTTATAAAGATAATAATATGTAAAAAATTTAGATGAATTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Reckle, Philipp
APPLICANT: Rebisching, Coringe
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF/5-30306/A/CGC1976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 186, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
TELEPANE: 919-541-8689
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEO ID NO: 1 SEQUENCE CHARACTERISTICS: LEGUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                             406 agtaataa 413
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US-08-998-416-186
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                                        646 TTATGTTCAAGACATGCAGGAAATATGATTCCAGATAATGATAAAAATTCAAATTATAAA 705
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APPLICANT: PACLECLI, EDZO
APPLICANT: de Taisne, Charles
APPLICANT: draisne, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48.8; DB 1; Length 10
Pred. No. 0.024;
0; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Curtis, Morris & Safford, P.C. 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 454310-2570
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-010-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY/AGGNT INFORMATION:
NAMME: FORMATION:
NAMME: FORMATION S.
                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08257073
Patent No. 5766597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.28;
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TELEFAX: (212) 840-0712
TELEEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1884 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.2's
Best Local Similarity 47.4's
Matches 146; Conservative
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                                                                                                                                                                     406 agtaataa 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
US-08-257-073-8
                                                                                                                                                                                                                                                                                                US-08-257-073-8
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                                  Conservative
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              Similarity
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                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-998-416-288/c
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COUNTRY:
                               Matches 116;
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Query Match
Best Local S
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                                                                                                    636 atcacaaaccaataagtttaagcaatatatttactcagctattttacaagatttttataa 695
                                                                                                                                                                                                                            696 agaaaaatcttatattgatatcacaaaaattactaattacttcaagagtatgtgataaa 755
                                                                                                                                                                                                                                                             491 ATAAGAAATTAAAGTTAAAATTAATTATAATAATTCTTATAAAAAGTTAAATAT 432
                                                                                                                                                                                                                                                                                                756 gaaacgetataeteageaagagetetetaaatattttgagetaaaatetaeeeetagtat 815
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 195, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                Length 615;
            Score 48.6; DB 4; Length 6 Pred. No. 0.022; 0; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Scien
STREET: 9410 key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 195:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 TATATTAATTATTGATAAT 293
            Query Match 5.2%;
Best Local Similarity 49.2%;
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         876 gttattaataaatgatatt 894
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                  44 ATTATTTTAGTTGATGACGGTTCTACGGATAATTCTGGGGAAATTTGTGATGCTTTTATG 103
                                                                                                                                                                                                                                                      223 ttgaacaaagcggtgaaaatttctaagggagaatatattttagaatggatgctgatgat
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Length 844;
                                                                                                                                                                                                                                                                                                                                                                                                         283 atttcatatccaagtagatttgataagcaaattcgttttatggaggaaaa 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 ATCGTAAAAGAAAATATGATTGAAACTCTTTATCAGCAAGTCCAAGAAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
Score 47.6; DB 3;
Pred. No. 0.039;
0; Mismatches 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQU
TITLE OF INVENTION: AND USES THEREOF
UNMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 288, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NABER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
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Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Mohr, Christine
APPLICANT: Wedland, Jurgen
APPLICANT: Rechile, Philipp
APPLICANT: Rebischung, Corinne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 288:
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: PAG1241RP
US-08-998-416-288
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         653 ttaagcaatatatttactcagctattttacaagatttttataaagaaaatcttatattg 712
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                          0; Mismatches 175;
          REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                  4.9%; Score 46; 46.3%; Pred. No.
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; Sequence 10, Application US/08990571
; Patent No. 6214971
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ATTORNEY AGENT INFORMATION:
ATMAR: Maki, David J.
REGISTRATION NUMBER: 31,392
31,392
                                                                                                                                    LENGTH: 3701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                     Best Local Similarity 46.3
Matches 151; Conservative
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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CITY: Seattle
STATE: Washington
                                                                                                                                                                                                     linear
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US-08-845-258-10
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                     Length 837;
                                   Score 47.4; DB 4; Length 8 Pred. No. 0.043; 0; Mismatches 296; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 CAAATAATTAATTAATAATAATAATAATAATAATAATAAA 75
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08845258 Patent No. 6183976
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                                   5.0%;
illarity 43.2%;
Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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STATE: Washington
COUNTRY: USA
ZIP.
                                                        Similarity
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US-08-845-258-10/c
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                                                                             Matches 225;
                                   Query Match
Best Local 9
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TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 3701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ADDRESSEE: No. 62392
                                                                                                             ; TOPOLOGY: linear
US-08-723-142A-10
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                     Gaps
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Loughton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSI
TITLE OF INVENTION: AND PREATMENT OF B. MICROTI INFECTION
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                 DB 4; Length 3701;
                                                                                                                                                                               Score 46; DB 4; Length 370 Pred. No. 0.11; 0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CANAGEM FELLIAND DATE: US/08/723,142A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426
TELECOMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttaatattttagtactgaaattgttt 918
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; Sequence 10, Application US/08723142A
; Patent No. 6306396
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-
             INFORMATION FOR SEQ ID NO: 10.
SEQUENCE CHARACTERISTICS:
LENGTH: 3701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                             4.9%;
(206)682-6031
                                                                                                                                                                                                  Best Local Similarity 46.3
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND E
STREET: 6300 Columbia
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STATE: Washington
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US-08-990-571-10
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 TELEFAX:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
                                                                                                                                                                                                                                                                                  0; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 6239264artis Corporation
                                                                                                                                                                                                                                  Score 46;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQU
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 893 ttaatattttagtactgaaattgttt 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 TTAAATTATCTATACTGATATATTT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1137, Application US/08998416 Patent No. 6239264 GENERAL INFORMATION:
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T: Pohlmann, Rainer
T: Steiner, Sabine
T: Mohr, Christine
T: Wendland, Jurgen
T: Knechtle, Philipp
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Best Local Similarity 46.3%;
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HATORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 34,241

REGISTRATION NUMBER: PF/5-30306/A/CGC1976

FLEEPOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8689

INFORMATION FOR SEQ ID NO: 1137:

SEQUENCE CHARACTERISTICS:

LENGTH: 636 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORGANISM: PAGI692RP

US-08-918-416-1137
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Search completed: August 2, 2002, 13:28:36 Job time: 9682 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 31, 2002, 18:56:25 ; Search time 13.52 Seconds (without alignments) 896.392 Million cell updates/sec Run on:

US-09-900-038A-1 1590 1 MNYSIIMSVYNEPLNYVRDS......LINDINILVLKLFGGEKQSD 313 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Y060_MYCPN EXOU_RHIME EX5C_BUCAI CSBB_BACSU SYV_YEAST CGED_BACSU BPS2_ACIAM MUTL_BORBU PDR6_YEAST YCF18_MYCTU RF18_MYCTU	ALLUNMENTS T 1 YAS7_METJA YAS7_METJA STANDARD; PRT; 290 AA. 15-50L-1998 (Rel. 36, Created) 16-0CT-2001 (Rel. 39, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 16-0CT-3001 (Rel. 40, Last annotation update) MAJ1057. MAY 2000 (Rel. 40, Last annotation update) MAJ1057. Archaea: Euryarchaeota; Methanococcales; Methanococcaceae Methanococcus. Archaea: Euryarchaeota; Methanococcales; Methanococcaceae MRCHAROCOCCUS.	ATCC 43067; 1689087; 16.J., Zhou L., Fleischn 11zGerald L.M., Clayton B.A., Tomb JF., Adams Weinstock K.G., Merrid M., Weidman J.F., Fuhrm M., Metars M.A., Kaine B.P. Smith H.O., Woese C.R., of the methanogenic arci of the methanogenic arci smith H.O., Woese C.R., of the methanogenic arci smith H.O., Woese C.R., of the methanogenic arci list con methanogenic arci smith H.O., Woese C.R., of the methanogenic arci list con	EMBL; UG/5549; AAB99061.1; TUGSP; MJ1057; TIGR; MJ1057; InterPro; IPR001173; Glycos_transf_2. InterPro; IPR001173; Glycos_transf_2. Hypotherical protein; Transferase; Complete proteome. SEQUENCE 290 AA; 35099 WW; 3F6A1B221C420D74 CRC64; SEQUENCE 290 AA; 35099 WW; 3F6A1B221C420D74 CRC64; TY Match 127.5%; Score 437.5; DB 1; Length 290; t Local Similarity 35.2%; Pred. No. 1.7e-22; ches 99; Conservative 58; Mismatches 101; Indels 23; G 4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL
6.7 299 1 6.7 342 1 6.6 1070 1 6.6 1324 1 6.5 1324 1 6.5 1324 1 6.5 1081 1 6.5 1081 1 6.4 1275 1	STANDARD; (Rel. 36, Cree (Rel. 39, Last (Rel. 40, Last cosyl transfer cosyl transfer is jannaschii. yarchaeota; Me	FROM N.A. AL.1 DSM 2661 / 96337999; Pubmed-e 10. Blake J.A.; E.A.R., Dougherty E.A.R. Dougherty E.A.R. Eraber B.F. E.Y. Fraser C.M.; P.Y. Fraser C.M.; E. Geophers Septence 9.00 Septence 773:1058-1073(1999 11.1"; E. Swiss Institute Pean Bloinformation Interpretations Into Profit institute Into Into Into Into Into Into Into Into	HBL; U67549; AAB99061.1; - GR; P39621; 10G8. GR; M1057; - tterPro; IPR001173; Glycos, trans there is a protein; Trans COUENCE 290 AA; 35099 M Match 27.5%; Local Similarity 35.2%; Hes 99; Conservative 4 SIIMSVYNEPLNYVRDSVESIL :: :: :: ::VWATYNEPEKYLKESIESIX 64 LNEENIGLASSLNKAVKISKGE
34 106.5 35 106 37 104.5 38 104.5 39 104 40 104 42 103.5 43 102.5 45 102.5	JUT 1 2_METJA YA57_METJA STA Q58457; 15-JUL-1998 (Rel. 30-MAY-2000 (Rel. 16-OCT-2001 (Rel. MJ1057. Methanococcus jann Archaea; Euryarcha Methanococcus. NCRI TAXTD=2190.	SEQUENCE FROD SEQUENCE FROD SEQUENCE FROD STRAIN-JAL-1 MEDLINE-9633 Bult C.J. W Werlavage A.J. Verrebeck R., Scott J.L., Cotton M.D., Cotton M.D., Complete gel jannaschili "Science 273":	EMBL; U67549 HSSP; P39621 TIGE; M1057 InterPro; IPP Pram; PF0053 Hypothetical SEQUENCE 2 Query Match Best Local Simi Matches 99; 4 SIIMSVY
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DFWIRCIANDYKFDIIEEFLLKYRIPNRDNYLSRIKKQKLYSYYT-LKTHWKNKKHFCNN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE—95350630; PubMed=7542800; Richard R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Shilley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                   IDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRDLVPVEDY
                                                                                  IDENGNIL-KEFKPEK-YKFKEIKKYFFKEHLTVHPSMMVKSKILKKLKYDEKLIRSQDY
                                                                                                                     DFAIRGALADFKIGLLNKVLLQYRL--NENGISQTNKFKQYIYSAILQDFYKEKSY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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                                                                                                                                                                                                                                                                                                                 YE78_HAEIN STANDARD; PRT; 323 AA. 057287; 005077; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Putative 91ycosyl transferase H11578 (EC 2.-.-).
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Pred. No. 6.5e-11;
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29.0%;
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Best Local Similarity
Matches 93; Conserv
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175
                                                                                                      185
                                                                                                                                                                                                                                                                         241 ITYYLNKIGIDIKVINSVSLLEIYHVDKSNKVLKSILYEMYMSLDKYTITSLLHFIKYHL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MELSCHMann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scort J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                       IDQKG-NLVYKQRESNKIY----LTNDIRKMLLNRSILAHPTWCVKKKVF--DKLMGYRD
                                                                                                                                            176 LVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQ---
                                                                                                                                                                                                                               -DFYKEKSYIDITKITN----SKY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McLaughlin R., Abu Kwaik Y., Young R., Spinola S., Apicella M.; "Characterization and sequence of the 1sg locus from Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase HI1695 (EC 2.-.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U32842; AAC23341.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
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us-09-900-038a-1.rsp

Pred. No.

Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                  118 TLIELIDOKGNLV-YKORESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRDL 176
                                                                                                                                                                                                             60 IKILLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN--SLDFSA 117
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bugert P., Geider K.;
"Molecular analysis of the ams operon required for exopolysaccharide
                                                                                                                                                                               1 MKFSVLMSLYIKENPQFLRECFESLVAQTRQADEIVLVFDGVVTPDLEFVVTEFE-TKLP
                                                                                                                                                                                                                                                                                          177 VPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKEKSY
                                                                                                                                                 1 MNYSIIMSVY-NEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
101-NAY-2000 (Rel. 39, Last annotation update)
Amylovoran blosynthesis glycosyl transerase amsE (EC 2....).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Exopolysaccharide synthesis; Transferase; Glycosyltransferase.
SEQUENCE 266 AA; 30748 MW; 163268A4210EB47B CRC64;
                                                                                       Length 267;
                                                                                                                     Indels
V -> G (IN REF. 1).
D -> E (IN REF. 1).
F -> S (IN REF. 1).
A2F1A0532737DBC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             237 IDITKITHYFQEYVIKKRYTQQELSKYFELKSTPSITIRKLY 278
                                                                                                                                                                                                                                                                                                                                                                                                                         LGIOGLLSGLFTFALR ------FGSRLLPTSLLKKLY 261
                                                                                    13.0%; Score 206.5; DB 1; 24.8%; Pred. No. 3.4e-07; ive 57; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-9531933; PubMed-7596293;
26 V
46 D
49 F
30770 MW;
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                                                                                                                    70; Conservative
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26
46
49
267 AA;
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Q46635;
CONFLICT
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SEQUENCE
                                                                                         Query Match
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DB 1; Length 266;

Score 199.5;

12.5%;

Query Match

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                                   12;
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAVIEFDEHG----KERLKRLPLSNNDIHEFARMKNPFNH--MCV----VFRKDKVISAGS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KILL--NEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSA 117
                                                                                                                                                                                                                                                                                                      PLVIVPLEKNLGLGKALNAGLERCTHNVVARMDTDDICLPERFEKQISYMESHPEVVLSG 117
                                                                                                                                                                                                                                                                                                                                                                             118 TLIELIDOKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVF--DKLM---G 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 YRDLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95350630; PubMed-7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., McKenney R.D., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shilley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Finchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C.,
                                       Gaps
                                                                                                   YSIIMSVYN--EPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRI 60
                                                                                                                                                                   57
                                                                                                                                      2 FSVLISLYNKEKPEN-LEQCLESLHQQTLNADEJVLVYDGPVSESLKAVATRWA---NLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McLaughlin R., Abu Kwaik Y., Young R., Spinola S., Apicella M.; "Characterization and sequence of the lsg locus from Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus
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                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M94855; AAA24982.1; -.
EMBL; U32842; AAC23342.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YG96_HAEIN STANDARD; PRT; 294 AA. 048214; 005082; Created) 16-CCT-2001 (Rel. 40, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) 17-CCT-2002 (Rel. 41, Last
                               Mismatches 107;
9.9e-07
                               48;
28.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 EKSYIDIT---KITNYF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 LKLALKQTGFIRGTLYF 242
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496-512(1995).
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SEQUENCE FROM N.A.
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YG96_HAEIN
                                   Matches
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  or send an email to license@isb-sib.ch)
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Science 269:496-512(1995).
                                                                                                                                      Query Match
Best Local Similarity 23.77
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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SDQTLTIEILE 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 LINDINILVLK 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
Y868_HAEIN
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                                                                                                                                                                                                                              15;
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-!- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING MINOR TEICHOIC ACIDS.
                                                                                                                                                                                                                                                                                                     60 IKILLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN---SLDFS 116
                                                                                                                                                                                                                                                                                                                   117 ATLIELIDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRD- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 TQKAIDYIREHYVKTVEQARNF-DIN--ASYILAYPHIMNLSRKAAKYYFDIFKKTKSI- 270
                                                                                                                                                                                                                                                                   3 SIIVPSYNRKAE-VPALLESLTQQTSSNFE-VIIVDDCSK------ERVVVEGSYSFP 52
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                    4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNR---- 59
                                                                                                                                                                                                                                                                                                                                                                     LVPVEDYDFAIRGALADFKIGLLNKVLLQ-----YRLNE------NGISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 TNKFKQYIYSAILQDFYKEKSYIDITKITNYFQEYVIKKRYTQQELSKYFEL-KSTPSIT
                                                                                                                                                                                                                             67;
                                                                                                                                                                                                    Score 196.5; DB 1; Length 294; Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                              Indels
                                              C -> Y (IN REF. 1).

S -> R (IN REF. 1).

T -> A (IN REF. 1).

C -> R (IN REF. 1).

C -> R (IN REF. 1).

V -> I (IN REF. 1).

V -> I (IN REF. 1).

I -> V (IN REF. 1).

B -> S (IN REF. 1).

B -> S (IN REF. 1).
               transf_2; 1.
Transferase; Glycosyltransferase;
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                                                                                                                                                                                                                             Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Minor telchoic acids biosynthesis protein ggaB.
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IPR001173; Glycos_transf_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 --KQFIITLVILISP---KLAIN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 IRKLYICLYLYFKSPLVRRLLIN 296
                                                                                                                                                                                                   12.4%; Scilarity 25.1%; Pr
Conservative 60;
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(Rel. 32, Last sequ
(Rel. 40, Last anno
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Μ
             Pfam; PF00535; Glycos_transi
Hypothetical protein; Transi
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                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 81; Conserv
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                                    Complete proteome
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01-NOV-1995
16-OCT-2001
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P46918;
                                              CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 -PNNI-VYAKKQNGGVSSARNYGLKYAEGRYIQFLDPDDLVSEGTFENVLNFFDEHKNEI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 SATLIELIDQKGNLVYKQRESNKIYLTN--DIRKMLLNRSILAHPTWC----VKKKVFDK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 DIVAIPIFFAEGR-TGEHNLNNKFSSTRILDVEKE--PHHILTH---CCSTFIKKDALKN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NYSIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVI----DNPSRGDL--KQFLTEYSV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95350630; bubMed=7542800; Richard F KW20; bubMed=7542800; Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Ferlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Sprigss T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|:|| :|| | | : :::|||:|||: || | :| |:| :: |:: :|
9 DFSVIMPIYNVEL-YLTEAIESIINQTI-GFENIQLILVNDDSPDKSEIICKEYAQKY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 LMGYRDLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGIS--QTNKFKQYIYSAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 QELSKYFE---LKSTPSITIRKLYICL-------YLYFKSPLVRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 QDFYKEKSYIDITKITNY-----FQEYVI---------KKRYTQ----
                                                                                                                                                                                                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                             Length 900;
                                                                                                                                                                                                                                                                                                                                             12.1%; Score 192; DB 1; Length 90 23.7%; Pred. No. 1.4e-05; Live 69; Mismatches 130; Indels
EMBL; U13979; AAA73513.1; -.
EMBL; Z99122; CAB15585.1; -.
Subtilist; BG11192; ggaB.
InterPro; IPRO01173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 900 AA; 107154 MW; FA66495488C2C62F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               057022, P9636;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative 91ycosyl transferase H10868 (EC 2....).
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Complete proteome
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P39621;
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     SO PRESENTANT OF THE PROPERTY 
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifiled and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIR-KI2 / MDIG55.
STRAIR-KI2 / MDIG55.
SOFIA H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Excharichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes ";
Nucleic Acids Res. 22:226-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 FTPTNQGPAAARNIGLEKAQGDYITFLDSDDFIANDKLEKQLNFMLQN------HLV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 MTHGNVAFCDLEGNQIKLVTTSKKIDYLTLLQGNQFKIMTVLVERESI-KLLRFPN-IKH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 DQKGNLVYKQRESNKIYLTNDIRKM----LLNRSILAHPTWCVKKKVFDKLMGYRDLVPV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 EDYDFAIRGALADFKIGLL--NKVLLQYRLNENGISQTNKFKQY1YSAILQDFYKEKSYI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 SIIMPVYNAEC-YLNQGILSCLNQSYQNIE-LILIDDGSTDKSIEIINNIIDKDKRVKLF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE-89174812; PubMed-2647748;
Aronson B.D., Somerville R.L., Epperly B.R., Dekker E.E.;
"The primary structure of Escherichia coli L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%; Score 189; DB 1; Length 25 27.0%; Pred. No. 4.6e-06; Ive 53; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                        Interpro: IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                             28915 MW; A5D8220129782E98 CRC64;
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                                                                                                                                                                                                                                      EMBL; U32768; AAC22526.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 GVVKSIYYFILY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 DITKITNYFQEY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                  HSSP; P39621; 1QG8.
                                                                                                                                                                                                                                                                                                                                                                                                          250 AA;
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SEQUENCE 250 AA
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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 ------LLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 ROGNKNLNY-------QRHYIKITRLLEKLNRNYADKIMIYPEFHQOITYEALRVC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKI- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 KYYAENYPHVRLLHQANAGASVARNRGIEVATGKYVAFVDADDEVYPTMYETLMTMALED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 --CVKKKV-FDKLMGYRDLVPVEDYDF-AIRGALADFKIGLLNKVLLQYRLNENGIS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 SLDFSATLIELIDOKGNLVYKQRESNKIYLTN-----DIRKMLLNRSILAHPTW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 DLDVAQCNADWCFRETGETWQSIPTDRLRSTGVLTGPDWLRMGLSSRRWTHVVWMGVYRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QTNKFKQYIYSAILQDFYKEKSYIDITKI-----TNYFQEYVIKKRYTQQ----ELSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 344;
J. Biol. Chem. 264:5226-5232(1989).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EcoGene; EG11266; yibb.
InterPro; IPR001173; Glycos_transf_2.
Pfam: PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IN REF. 2).
R -> G (IN REF. 2).
9B5DABFE86D5457A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 182.5; DB 1;
; Pred. No. 1.8e-05;
67; Mismatches 117;
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01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 FELKSTPSITIRKLYICLYLYFKSPLVRRLLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 HAVRKEPDILTRQRMIA--EIFTSGMYKRLITN
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MEDLINE-95020537; Pubmed-7934828;
                                                                                                                                                                                                                                                                                                               EMBL; U00039; AAB18592.1; -.
EMBL; AE000439; AAC76639.1; -.
EMBL; X06690; CAA29885.1; -.
PIR; A30268; Q3ECTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis.
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NCBI_TaxID=562;
                         Bacteria; Pr
Escherichia.
                                                                                     STRAIN=K12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KILLNE-----ENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFME--- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 ENSLDFSATLIELIDQKGNLVYKQRESNKIYLTNDIRKMLLNRSIL------AHPTW-- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---CVKKKVFDKLMGYRDLVPVEDYDFAIRGALADFKIGLLNKVLLQYRL 207
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 SVIMTSYNKS-DYVAKSISSILSQTFSDFELFIMDDNSNEETLNVIRPFLN----DNRV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDL---KQFLTEYSVVDNRI 60
                                                6
                                                                                                                                                                                                                                                                                                                                                                                Subtilist; BG10609; spsA.
InterPro; IPR001173; Glycos_transf_2.
InterPro535; Glycos_transf_2; 1.
Transferase; Glycos_transferase; 3D-structure; Complete proteome.
DISULFID 155 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 PCAIDHCSVMHRYSVLEKVKEKFGSYWDESP-----AFYRIG---DARFFWRV
                                              "Bacillus subtilis genome project: cloning and sequencing of the
kb region from 325 degrees to 333 degrees.";
MOL. Microbiol. 10:371-384(1993).
Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
Hullo M.F., Ionoscu M., Lubochinsky B., Marcelino L., Moszer I.,
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 175; DB 1; Length 256; 24.6%; Pred. No. 4e-05; ive 45; Mismatches 71; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative colanic acid biosynthesis glycosyl transferase wcaA.
                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 NENGISQINKFKQYIYSAILQDFYKEKSYIDITKIIN---YFQEYVIKK 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                           C20EA9627F5D536B CRC64;
                                                                                                                                                                                       PATHWAY: SPORE COAT POLYSACCHARIDE BIOSYNTHESIS.
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Best Local Similarity 24.63
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                               Stevenson G., Andrianopoulos K., Hobbs M., Reeves P.R.;
"Organization of the Escherichia coli K-12 gene cluster responsible for production of the extracellular polysaccharide colanic acid.";
J. Bacteriol. 178:4885-4893(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-K12 / MG1655,
MEDLINE-9742617; PubMed-9278503;
Blattner Fr., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Forna N.T., Burland V.,
Gregor J., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
A 460 kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
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Pfam; PF00535; Glycos_transf_2; 1.
Lipopolysaccharide biosynthesis; Transferase; Complete proteome.
SEQUENCE 279 AA; 33035 MW; 75F74D30026E327A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mau B., Shao Y.;
The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: TO R.MELILOTI EXOO.
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les 75; Conservative
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DYVCQ--GEVYSQPASLPLYPKSPYSRRLFYKRNIIGNQVFTWAWRFKECLFD-----TE 175
                         176 LVPVEDYDFAIRGAL---ADFKIGLLNKVLLQYRLNENGI---SQTNKFKQYIYSAILQD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
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                                                   LKAAQDYDIFLRMVVEYGEPWKVEEATQIL---HINHGEMQITSSPKKFSGYFH-----
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Rhizobiaceae; Rhizobium.
NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-97305956; PubMed=9163424;
Fretherq C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal
Perret X.;
"Molecular basis of symblosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
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Pfam: PF00535; Glycos_transf_2; 2.
HypothetLcal Protein: Plasain: Page Protein: Plasain: SEQUENCE 909 AA: 102827 MW; 3985D69722F43962 CRC64;
                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 102.8 kDa protein Y4GI.
                                                                                               FY-KEKSYID-ITKITNYFQEYVIK-KRYTQQEL 260
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                                                                                                                                                                                                                                                                        (strain NGR234)
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Best Local Similarity
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P55465;
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Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Danchin A.;
"Bacillus subtilis genome project: cloning and sequencing of the
Kb region from 325 degrees to 33 degrees.";
Mol. Microbiol. 10:371-384 (1993).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
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EMBL; 299123; CAB15824.1; -.
PIR; S39711; S39711.
Subtlist; BG10602; ywdF.
Interio: IRR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2, 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 AA; 30616 MW; DD8428F7016EC9B3 CRC64;
                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative glycosyl transferase ywdF (EC 2....).
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STANDARD;
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Best Local Similarity
Matches 68; Conserv
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                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                     Bacillus subtilis.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=1423;
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YS86_ANASP
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323 AA

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90264305; PubMed-2111805;
Holland D., Wolk C.P.;
"Indentification and characterization of hetA, a gene that acts early
in the process of morphological differentiation of heterocysts.";
J. Bacteriol. 172:3131-3137(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanbab A., Iriguchi M., Ishikwa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yabata S., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
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65; Mismatches 114; Indels
                                                                                                                                                                                         Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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Interpro; IPR001173; Glycos_transf_2.
Pfam: PF00555; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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                                       01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase alr2836 (EC 2.-.-).
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EMBL; AF031959; AAC32401.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21595285; PubMed=11759840;
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Best Local Similarity 20.00
Loca 61, Conservative
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19,
41,
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RESULT 14 YKCC BACSU

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InterPro; IrROU1173; Glycos_transf_2.
Pfam; PF0535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 VRDERLAGETK-----YPLKK----MLKLSMDGITTFSHKPLKLASYAGILMSGTGFLY 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 -VPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAI-----LQDF
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                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative glycosyl transferase ykcC (EC 2....).
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15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                             Bacillus subtilis
                                                                                                                                                                                                                                                            NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFAMILY.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Amylovoran blosynthesis glycosyl transerase amsB (EC 2.-.-).
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Pfam: PF00535; Glycos_transf_2; 1.
Exopolysaccharide synthesis; Transferase; Glycosyltransferase.
SEQUENCE 301 AA; 34788 MW; 99D0EE3080E6EC06 CRC64;
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Best Local Similarity 21.1%; Pred. No. 0.056;
Matches 62; Conservative 67; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                      STRAIN-EA1/79;
MEDLINE-9531933; Pubmed-7596293;
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                               Erwinia amylovora
                                                                                                                                                                                                                                               NCBI_TaxID=552;
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July 31, 2002, 18:51:04 ; Search time 17.53 Seconds (without alignments) 1715.685 Million cell updates/sec
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1 MNYSIIMSVYNEPLNYVRDS......LINDINILVLKLFGGEKQSD 313
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		glycosyl transfera	glycosyltanstates	alvoor) transfers	exopolysaccharide	qlycosyl transfera			hypothetical prote	teichuronic acid b	glucosyltransferas	exopolysaccharide	biosynthesis of te	hypothetical prote	hypothetical prote	o		glycosyl transfera	glycosyl transfera	minor teichoic aci	lacto-N-neotetraos	glucosyltransferas	hypothetical prote	probable qlycosyl	hypothetical prote	probable qlycosyl	hypothetical prote	lacto-N-neotetraos	glycosyl transfera
SUMMARIES		101167	A97168	B97168	B84114	T44330	G95948	н64130	AG2188	E84107	AB2092	D70036	A69728	E97757	AH2026	E90984	нв5829	E71703	G97777	E71690	н81970	AI2091	AG2189	E83022	C64175	G71148	G71153	D81027	F95015
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% Query Match	37 1	73.1	10	•		•	17.0	16.6	15.8	15.5	•	13.9			13.7	13.7	13.7	13.7	•	13.6				13.1	13.0	٠	•	12.9	12.9
Score	421 5	747	3,400	317	300.5	282	271	264	251	246.5	221.5	221	220	220	218.5	218	218		216.5	215.5	215.5	212.5	210.5	208	206.5	206.5	205.5	205	204.5
Result No.		10	4 (*	4	· w	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

RESULT 2
H97167
91ycosyltransferase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum

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202. 202. 202. 203. 204. 205. 206. 206. 207. 207. 207. 207. 207. 207. 207. 207	33 202.5 12.33 202.5 12.33 202.5 12.33 202 12.33 202 12.33 202 12.33 196.5 12.33 196.5 12.33 196.5 12.33 196.5 12.33 196.5 12.33 196.5 12.40 190.5 140			sferase thanocco p-1996 H64431 h04124 coverbo	IRCIAND
	RESULT 133 333 333 333 333 333 333 333 333 33			1 13 DFA 113 D	68

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C;Accession: B84114
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B84114
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exopolysaccharide biosynthesis BH3714 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycosyltransferase [imported] - Clostridium acetobutylicum
C.Species: Clostridium acetobutylicum
C.Species: Clostridium acetobutylicum
C.Species: Clostridium acetobutylicum
C.Species: Glostridium acetobutylicum
C.Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C.Accession: B97168
R.Nolling, J.; Bratch, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A.Recession: B97168
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-333 < kUR>
A.Residues: 1-333 < kUR>
A.Residues: 1-333 < kUR>
A.Residues: GB.AE001437; PIDN:AAK80133.1; PID:g15025169; GSPDB:GN00168
A.Sterimental source: Clostridium acetobutylicum ATCC824
C.Genetics:
A.Gene: CAC2175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 F---GDVSREOKLEREHWYNVDLNNSESIESLFLENCYIAHPSVMMKMSVLKALGGYNLN 177
                                                                                                                                                             ISREHRGLVDSLNEGINIARGKYIARMDADDISINNRIEKQFEFLELNKDVDILGTRIEA 124
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                                                                                                             ---IDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYR-DLVP
                                                                                                                                                                                                                                                                                             179 VEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKEKSYID
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1larity 32.8%; Pred. No. 2.6e-13;
Conservative 53; Mismatches 91
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236 VKEKLKLKDFSYV 248
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Best Local Similarity
Matches 83; Conserv
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C:Species: Aspecies: Aspecies:
                                                                                                                                                                                                                                                  Solvent-Producing Bacterium Clc
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C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C; Accession: H97167
R; Nolling, J.; Benetch, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A. Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacte. A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: H97167
A; Molecule type: DNA
A; Residues: 1-333 < KUR>
A; Residues: 1-333 < KUR>
A; Residues: GB: AEC01437; PIDN: AAK80131.1; PID:q15025167; GSPDB:GN00168
C; Genetics: A; Generics: Clostridium acetobutylicum ATCC824
A; Gene: CAC2173
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; Pred. No. 1.6e-16;
62; Mismatches 92
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les 90; Conserv
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probable glycosyltransferase protein SMb21189 [imported] - Sinorhizobium meliloti
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C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C; Accession: T44330
R; Yamaaaki, S.; Shimtu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
Gene 237, 321-332, 1999
A; Title: The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are close
A; Accession: T44330
A; Accession: T44330
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: DNA
A; Residues: 1-340 < YAM>A; Residues: 1-340 < YAM>A; Cross-references: EMBL; AD012957; NID:g4115688; PIDN:BAA33634.1; PID:g3721684
A; Molecule type: DNA
A; Residues: 1-271 <STO>
A; Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07433.1; GSPDB:GN00
A; Experimental source: strain C-125
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GTLAYLFRETPSKNKMMCHPEDHDSLIIRLLFSVCFIHPVVMIRKSVLDQL----DY 172
                                                                                                                                                                                                                                                                                                                                                LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENS-LDFSATLIEL 122
                                                                                                                                                                                                                                                                                                                                                                                    64 HNKNNRGLSYSLAEGVSLAKAPWIARMDADDVSFKDRLAVQMDHVKAHSELDILGSYVID 123
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                                                                                                                                                                                                                                                                                     4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL
                                                                                                                                                                                                                                                                                                                                                                                                                               123 IDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGY-RDLVPVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI
                                                                                                                                                                                    Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 340;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: Neisseria meningitidis glycosyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycosyl transferase homolog [imported] - Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 VPVEDY----DFAIRGALAD-FKIGLLNKVLLQYRLNENGIS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSA
                                                                                                                                                                               ; Score 300.5; DB 2;
; Pred. No. 2.3e-12;
41; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.7%; Score 282; DB 2; 36.9%; Pred. No. 4.6e-11; tive 35; Mismatches 77;
                                                                                                                                                                               18.9%;
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                                                                                                                                                                                                                        Conservative
                                                                                                                                                                               Query Match
Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 82; Conserv
                                                                                                                    A; Gene: BH3714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
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Accession: Heamophilus influenzae (Strain Rd KW20)

C;Species: Haemophilus influenzae
C;Dectes: Name No. 1990
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
G;Gorayne, J.D.; Sontt, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Accession: H64130
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                          A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-367 <kUR>
A:Experimental source: strain 1021, megaplasmid psymB

B:Galibert, F: Finan, T.M.: Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.

L.: Hyman, R.W.: Jones, T.
Science: 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A:Teference number: A:Reference number: A:Reference number: A:Reference number: A:Reference number: A:Reference number: A:Reference number: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-323 <TIGR>
A; Cross-references: GB:U32832; GB:L42023; NID:g1574421; PIDN:AAC23227.1; PID:g1574422
C; Superfamily: Neisseria meningitidis glycosyl transferase A
                                                                                                                                                      Her
C; Species: Sinorhizobium mellioti
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C; Accession: 695948
Frinan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; He
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A; Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing and A; Accession: 695948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIDOKGNLVYKORESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVF-DKLMGY-RDLVPV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIR-FMEENSLDFSATLIE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SIIMSVYN-EPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.6%; Score 264; DB 1; Lv 29.0%; Pred. No. 6.2e-10; ive 62; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.0%; Score 271; DB 2; 33.8%; Pred. No. 2.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDYDFAIRGALAD-FKIGLLNKVLLQYRLNENGISQTNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:| | :|| | :|| | : || EDFDLFRR--IADREPOVHMIDEALVAYRIHEDSVTSKHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Matches 93; Conservative
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13;

Gaps

52;

Indels

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teichuronic acid biosynthesis tuaG [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: 10-10-10
C;Accession: E84107
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Residues: 1-257 <STO>
A;Resperimental source: strain C-125
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 DOKGNLVYKORESNKIYLT--NDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRDLVPVED 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 -YDFAI-----RGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 329;
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C;Species: Anabaena sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 3.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.5%; Score 246.5; DB 2
Best Local Similarity 29.6%; Pred. No. 6.1e-09;
Matches 80; Conservative 59; Mismatches 96
| | ::: | | : ---SIAINLMRWFGADGYS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYIDITKITNYFQEYVIK -- KRYTQQELSK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKLSFVKSGWYFMHYVWRSLKKY----LSK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.9%;
24.5%;
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Best Local Similarity
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A; Status: preliminary
: || |
282 QEYIRL---
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                                                                                                                           10
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Anabaena sp. Anabaena sp. Anabaena sp. Strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AG2188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Readdues: 1-321 <KURN
A;Cross-references: GB:BAO00019; PIDN:BAB74761.1; PID:g17132156; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                          66 SNKYNLGFINSLNIGLGCFSGKYFARMDADDIAKPSWIEKIVTYLEKNDHITAMGSYLEI 125
                                                                                                                                                                                                                                                                                                            186 YPYAEDYKFWSEVSRLGCLANYP-----EALVKYRLHGNQTSSVYNHEQNETAKKIKREN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENS-LDFSATLIEL 122
                                                                                                                                                                                                                                                                             123 IDQKG-NLVYKQRESNKIY----LTNDIRKMLLNRSILAHPTWCVKKKVF--DKLMGYRD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ITYYLNKIGIDIKVINSVSLLEIYHVDKSNKVLKSILYEMYMSLDKYTITSLLHFIKYHL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSATLIEL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KEKSY-----IDITKITNYFQEYVIKKRYTQQELSKYFELKSTPSITIR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 ATASQDLQVLKNKSYGFTYLCLAWKPLQSFQKDYQKSREFCQQAVAYY-----PSLRFS 281
                               63
                                                            4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein alr3062 [imported] - Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SY----VEDWDMWLRIAISYDFKV--VKEALVYYRQRSNSASKNWEAMAHSFAIVIEKAF
                               SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL
                                                                                                                                                                                                                                                                                                                                                                                                  LVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 -DFYKEKSYIDITKITN----SKY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 IDQKG---NLVYKQRESNKIY--LTN----DIRKMLLNRSILAHPTWCVKKK-VFDKLMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.8%; Score 251; DB 2; I
Best Local Similarity 24.6%; Pred. No. 4.2e-09;
Matches 83; Conservative 85; Mismatches 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 --FELKSTPSIT---IRKLYI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 ELFDLKONLKIIKKFIRKINV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: alr3062
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Matches 78; Conservative 71; Mismatches 129; Indels 41; Gaps 13; Qy 4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFITVIDNPSRGDLKQFLTEYSVVDNRIKIL 63 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	Db 124 MLVFDEFGVRGARILPSVPEPGIMAKGTPFCHGTIMMRAS 163 Oy 166 VFDKLMGYRDLVPVEDYDFAIRGALADFKIGLLNKVLLOYRLNENGISGTNKFKQYI 222 Ob 164 APPTIKYYSVPPPRAMPHOLIVIALPEPEPGPECHICAL
64 LNEENIGLASSLNKAVKISKGEVIFRMDADDISYPSRFDKQIRFMEENS-LDESATLIEL : : : : : : :	223 YSAILQDEYKEKSYIDITKITNYFOEVVIKKRYTQQELSKYFELKSTPSITIRKLYICLY
QY 123 IDOKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGY-RDLVPV 179	Qy 283 LYFKSPLVRRLL 294
Qy 180 EDYDFAIR-GALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKEKSYID 238	RESULT 13 A69728 Picerial of total of total of the contraction of the
OY 239 ITKITHYFQEYVIKKRYTQQELSKYFELKSTFSITIRKLYICLYLYFKSPLVRLLINDI 298 139 QLVHNHFALAQAVHLKYLARRAFFLKLFARVGVDFITRALISDW 282	subtilis subtilis #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
Oy 299 NILVLKLFG 307 1 : : : : : : : : : : : : :	R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
RESULT 12	A, Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Kotter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Kotter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Kotter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Kotter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Kotter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Kotter, P.; Kotter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Kotter, P.; Kotter
cyony exopolysaccharide biosynthesis homolog yveO · Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999	
C; Accession: D70036 B; Kunst, F.; Ogssaware, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A. Phriich C. D. Function D. T. Entist, D. Princeton	
Nature 390, 249-256, 1997 A; Authors: Foulger, D.; Fritz, C.; Fullta, M.; Fullta, Y.; Fuma, S.; Galizzi, A.; Gallen	
tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,	
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetellé Rieger, W.; Rivolta, C.; Rocha, E.; Roche, B.; Rosse, M.; Sadaie, Y.; Sato, T.; Scanlon, A.Authors. Schlaich, G. Schroter B. Schfinger F. Schinchi J. Schowska a. Schrot	
Akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Winters, P.; Yata, K.; Yata, K.; Yoshida, K.; Yata,	
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A:Reference number: A69580; MUID:98044033 A:Accession: D70036	Query Match 13.8%; Score 220; DB 2; Length 252; Best Local Similarity 27.9%; Pred. No. 3e-07; Matches 79; Conservative 45; Mismatches 87; Indels 72; Gaps 12;
A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA A:Molecule type: DNA A:Residues: 1-278 <kun> A:Cross-references: GB:299121; GB:AL009126; NID:92635827; PIDN:CAB15438.1; PID:el186121;</kun>	QY 4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
A,Experimental source: Strain 108 C;Genetics: A,Gene: yveo	QY 64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI 123
Query Match 13.9%; Score 221; DB 2; Length 278; Best Local Similarity 24.7%; Pred. No. 2.9e-07; Matches 77; Conservative 53; Mismatches 96; Indels 86; Gaps 11;	QY 124 DQKGNLVYKQRESNKIYLTNDIRKMLLNRSILA 156
Oy 4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLROFLTEYSVVDNRI 60	QY 157 HPTWCVKKVVFDKLMGYRDLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQ 214
Qy 61 KILLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN 111	QY 215 THKFKQYIYSAILQDFYKEKSYIDITKITHYFQEYVIKKR 254 : : : : : : : Db 212 SHKWKAAKKTWFVYREIERLHFMKATWCFVQYAKNAVKKR 251
Qy 112 SLDFSATLIELIDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKK 165	RESULT 14

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64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSATLIEL 122
                                                                                         123 IDQKGNLVYKQRESNKIYLTNDIRKMLLNRSIL---AHPTWCVKKKVFDKLMGY-RDLVP 178
                                                                                                                      233 YQARPAIGNHILHISIANLYKYLACKALQKPYSRSKGLAAVKFIWQYFLYDSS---RMRR 289
                                                                                                                                                                                                                       FSFENAGGNVSRNRGLNLAVGKFISFLDADDIWTPNKLESQLEALHNNPGFHVAYSWTDY
                                                                                                                                                                                      179 VEDYDFAIRGALADFKIGLLNK------VLLQYRLNENGISQTNKFKQYIYSAILQDF
                                                                                                                                                                                                                                                                                  YKEKS-----YIDITKITNYFQEYVIKKRYTQQE-----LSKYFELKSTPSITIRK
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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                                       Cipecies: Rickettsia conorii
Cipace: 30-Sep-2001 #text_change 30-Sep-2001
Cipace: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
Cipacession: B97757
Riogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MuID:21442074; PMID:11557893
A;Reference number: A97700; MuID:21442074; PMID:11557893
A;Reference preliminary
A;Molecule type: DNA
A;Residues: 1-604 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL02999.1; PID:g15619533; GSPDB:GN00173
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Anabaena sp.
A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AH2026
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A;Experimental source: strain PCC 7120
C;Genetics:
                      hypothetical protein RC0461 [imported] - Rickettsia conorii (strain Malish 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRDLVPVED-- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 IMISIASKNSIGGIDKELSKVRISGGTNTFMDPNKYSVGLIN--ITSYVLNDAYLSKFSP 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FK-QYIYSAILQDFYKEKSYIDITK--ITNYFQEYVIKKRYTQQELSKYFELKSTPSI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein all1766 [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
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                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 604;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.8%; Score 220; DB 2; Length 60
Best Local Similarity 25.8%; Pred. No. 9e-07;
Matches 77; Conservative 65; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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Best Local Similarity
Matches 75; Conserv
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A;Residues: 1-333 <KUR>
A;Cross-references: GB:E
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Sequence Seq

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APPLICANT: GOLSCHLICH, EM11 C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
FILING DATE: July 7, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.2%; Score 210.5; DB 1; 27.8%; Pred. No. 1.3e-11; ative 55; Mismatches 123;
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELERX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08312387B Patent No. 5545553 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 348 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 27.8°
Matches 86; Conservative
      MOLECULE TYPE: protein
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        7766666666666666666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-312-387B-3
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        July 31, 2002, 18:50:29 ; Search time 13.08 Seconds (without alignments) 584.496 Million cell updates/sec
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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/RCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/RCTUS_COMB.pep:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-312-387B-3
US-08-312-387B-11
US-08-683-456-3
US-08-683-456-3
US-08-683-458-3
US-08-878-360-3
US-08-878-360-3
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US-08-878-360-11
US-08-878-360-11
US-08-333-412-3
US-09-333-412-3
US-08-312-387B-5
US-08-312-387B-5
US-08-683-426-5
US-08-683-426-5
US-08-683-458-5
US-08-683-458-5
US-08-683-458-5
US-08-683-458-5
US-08-683-458-5
US-08-683-458-5
US-08-683-458-5
US-08-878-360-12
US-09-333-412-12
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Total number of

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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Minimum I Maximum I

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Result . 9 15;

Gaps 63

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US-08-746-682A-10 US-08-961-083-196 US-08-961-083-202

210.5 210.5 210.5 210.5 2210.5

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SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                                                                                                                                                                            64 AQAQNSGLIPSLNIGLDELAKSGGGGGFYIARTDADDIASPGWIEKIVGEMEKDRSIIAM 123
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                                                                                                                                                                                                                                  SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT----QQELSKYFEL--KSTPSITIRKL
                                                                                                                                      MGY ---RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08683426
Patent No. 5705367
GENERAL INFORMATION:
APPLICANT: GCTSCALICA, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/683,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.2%; Score 210.5; DB 1; Best Local Similarity 27.8%; Pred. No. 1.3e-11; Matches 86; Conservative 55; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSTEICATION: 536
PION APPLICATION DATA:
APPLICATION UNBER: 08/312.387
FILING DATE: September 26, 1994
CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: Jackson ESQ., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: All Hackensack Avenue CITY: Hackensack Avenue CITY: Hackensack COUNTR: USA ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 201 343-1684
TELEFAX: 301 343-1684
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
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.....TERISTICS:
TYPE: amino acids
TOPOLOGY: lin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) MOLECULE TYPE: protein US-08-683-426-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                       278 YICLYLYFK 286
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                         64 LNEENIGLASSLNKAV-KISK-----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
64 LNEENIGLASSLNKAV-KISK----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
                                                                                         SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                                      171 MGY---RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
                                                                                                                                                                                                                                                                          224 SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT----QQELSKYFEL--KSTPSITIRKL 277
                                                                                                                                                                                                                                                                                                                       235 -EIAQGIQK-----TARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08312387B
Patent No. 554553
Patent No. 554553
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOLSCHLICH, Emil C.
APPLICANT: GOLSCHLICH, EMIL C.
TITLE OF INVENTION: GLYCOSYLFRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCES ADCRESS:
CORRESPONDENCE ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 348;
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MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
FILING DATE: Unly 7, 1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.2%; Score 210.5; DB 1;
11arity 27.8%; Pred. No. 1.3e-11;
Conservative 55; Mismatches 123;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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amino acid
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 86; Conserv
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64 AQAQNSGLIPSLNIGLDELAKSGGGGGEXIARTDADDIASPGWIEKIVGEMEKDRSIIAM 123
                                                                                                                         116 SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                                                                 64 LNEENIGLASSLNKAV-KISK-----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
6 SVLICAYNVE-KYFAQSLAAVVNQTWRNLDILIVDDGSTDGTL-AIAKDFQKRDSRIKIL 63
                                                                                                                                                                                                                                                                                                                           224 SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT----QQELSKYFEL--KSTPSITIRKL
                                                                                                                                                                                                             171 MGY----RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEGUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/683,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match · 13.2%; Score 210.5; DB 1; Best Local Similarity 27.8%; Pred. No. 1.3e-11; Matches 86; Conservative 55; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600-1-095A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08683458 Patent No. 5798233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 348 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07601
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64 LNEENIGLASSLNKAV-KISK----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
                                                                               116 SATLIELIDOK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                            64 AQAQNSGLIPSLNIGLDELAKSGGGGGYIARTDADDIASPGWIEKIVGEMEKDRSIIAM 123
                                                                                                                                                                   171 MGY----RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
                                                                                                                                                                                                                                                       SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT----QQELSKYFEL--KSTPSITIRKL 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: GLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: US/08/683,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.2%; Score 210.5; DB 1; 27.8%; Pred. No. 1.3e-11; tive 55; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             __: _ _ :: : = ::: :: ::
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PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: September 26, 1994
CLASSIFCATION: 536
ATTORNEY, AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELECHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08683426 Patent No. 5705367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201343-1684
TELEX: 133521
INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
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STATE: New Jersey
COUNTRY: USA
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287 RRFLYQCFK 295
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                                                                                         116 SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                                                                                                                                MGY---RDLVPVEDYDF----AIRGALADFKIGLINKVLLQYRLNENGISQTNKFKQYIY 223
                                                                                                                                                                                                                                                                                                            235 -EIAQGIQK-----TARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERA 286
4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                   6 SVLICAYNVE-KYFAQSLAAVVNQTWRNLDILIVDDGSTDGTL-AIAKDFQKRDSRIKIL 63
                                                                                                                                                                  224 SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT----QQELSKYFEL--KSTPSITIRKL
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Patent No. 5798233
GENERAL INFORMATION:
APPLICANT: GOTSCHAICH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 210.5; DB 1;
Pred. No. 1.3e-11;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
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STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
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27.8%;
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
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3%: linear
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Best Local Similarity
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                                                                                                                                                              SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                                                                                                                                                                     171 MGY---RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
                                                                                                                                                                                                                                                                                                                                                             184 LRYDTERDW--AEDYQFWYDVSKLGRLAYYP----EALVKYRLHANQVSSKHSVRQH-- 234
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                                                                    4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
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Patent No. 5945322
GENERAL INFORMATION:
APPLICANT: GCTSCALLICH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
55; Mismatches 123; Indels
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CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/878,360
FILING DATE: 18-JUN-1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
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STREET: 411 Hackensack Avenue
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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amino acid
GY: linear
Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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86;
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SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE, POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A POLYGLYCOSYLTRANSFERASE
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                                                                                                                                                                                                                                                                                                                                                                                           235 -EIAQGIQK------TARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERA 286
                                                                                                                                                                                                                                                                                                                           64 AQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAM 123
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                                                                                                                                                                                                                             4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
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                                                                                                                                                             Indels
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APPLICANT: ROTH, STEPHEN
APPLICANT: BUCZALLA, STEPHANIE L.
TITLE OF INVENTION: METHOD OF TRANSFERRING AT LEAST TWO
TITLE OF INVENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYL
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENV
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE
NUMBER OF SEQUENCES: 8
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APPLICATION NUMBER: US/08/478,140B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                  13.2%; Score 210.5; DB 2; 27.8%; Pred. No. 1.3e-11; iive 55; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7188-017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (212) 790-9090
(212) 869-9741/8864
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TELECOMMUNICATION INFORMATION:
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NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                Query Match
Best Local Similarity 27.8%
Matches 86; Conservative
                               , MOLECULE TYPE: protein US-08-878-360-11
amino acid
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New York
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ZIP: 10036-2711
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                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                       64 LNEENIGLASSLNKAV-KISK-----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
                                                                                                                                                                                                                                                                                                                                                               171 MGY---RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                224 SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT----QQELSKYFEL--KSTPSITIRKL 277
                                                                              Gaps
                                                                                                                4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                        TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM NUMBER OF SOURCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                      Length 348;
                                  13.2%; Score 210.5; DB 2; Length 27.8%; Pred. No. 1.3e-11; tive 55; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFRAX 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/878,360 FILING DATE: 18-JUN-1997 CLASSIFICATION: 435
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FILING DATE: September 26, 1994
CLASSIFICATION: 435
ATORNET INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08878360 Patent No. 5945322 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,426
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                          86; Conservative
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                                                       Similarity
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                                  Query Match
Best Local S:
Matches 86
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FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION UNDBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
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ADDRESSEE: Klauber & Jackson
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  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New Jersey COUNTRY: USA
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Best Local Similarity 27.8
Matches 86; Conservative
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TITLE OF INVENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE, A
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                      64 LNEENIGLASSLNKAV-KISK-----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
                                                                                                                                                                                                                                                                                                                                       SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
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                                                                                                                                                                                                  45;
                                                                                                                                                             Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08478140B
Patent No. 6127153
GENERAL INFORMATION:
APPLICANT: JOHNSON, KARL F.
APPLICANT: ROTH, STEPHEN
APPLICANT: BOCZALA, STEPHANIE L.
TITLE OF INVENTION: METHOD OF TRANSFERRING AT LEAST TWO
                                                                                                                                                                                                  Indels
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COUNTRY: USA
ZIP: 10036-2711
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPTTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PATCHTIN Release #1.0, Version #1.30
                                                                                                                                                           DB 3;
                                                                                                                                                                                                55; Mismatches 123;
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                                                                                                                                                           Score 210.5;
Pred. No. 1.3
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1155 Avenue of the Americas
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FILING DATE: 07-UUN-1995
CLASSIFICATION: 435
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TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
                                                                                                                                                           13.2%; 27.8%;
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                       Query Match
Best Local Similarity 27.8<sup>†</sup>
Matches 86; Conservative
                                                                            ; MOLECULE TYPE: protein US-08-478-140B-3
                                                            linear
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                                                            TOPOLOGY:
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                                                                     Gaps
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Sequence 3, Application US/09333412
Patent No. 6342382
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL GENERALICANT: GOTSCHILCH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                     45;
         Length 348;
                                                                     Indels
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COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
13.2%; Score 210.5; DB 3; 27.8%; Pred. No. 1.3e-11; ive 55; Mismatches 123;
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FILING DATE: 15-Jun-1999
CLASSIFICATION: <UNKNOWN>
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64 LNEENIGLASSLNKAV-KISK----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
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Patent No. 554553
GENERAL INFORMATION:
APPLICANT: GOLESCHIICH, EMIL C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             13.2%; Score 210.5; DB 4; ilarity 27.8%; Pred. No. 1.3e-11; Conservative 55; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-09-333-412-11
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July 7, 1994
  REGISTRATION NUMBER: 26,742
                   REFERENCE/DOCKET NUMBER: 6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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Best Local Similarity
Matches 86; Conserva
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                                                                                                                                                                                                                                                                                                                                                                     4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09333412
Patent No. 6342382
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                        Length 348;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: 0.5/09/333,412
FILING DATE: 15-Jun 1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                    13.2%; Score 210.5; DB 4; 27.8%; Pred. No. 1.3e-11; tive 55; Mismatches 123;
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APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 411 Hackensack Avenue
CITY: Hackensack
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                          INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                 TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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                                                         TELEX: 133521
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                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 86; Conserv
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                              : 337 amino acids
amino acid
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Best Local Similarity 22.69
Matches 62; Conservative
SEQUENCE CHARACTERISTICS:
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                                                                                                                          MOLECULE TYPE: protein
                                                                                                     linear
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                                                                                                                                                            US-08-312-387B-12
                                                                                               TOPOLOGY:
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Sequence 12, Application US/08312387B

Sequence 12, Application US/08312387B

SEQUENCE 12, Experiment 
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.1%; Score 176.5; DB 1
22.6%; Pred. No. 1.6e-08;
ative 60; Mismatches 93
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ER: 600-1-095
600-1-095
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
FILING DATE: July 7, 1994
CLASSIFICATION: 435
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411 Hackensack Avenue
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO: 12:
                                                                                                                   TELEX: 13321
INFORMATION FOR SEO ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 337 amino acid
TYPE: amino acid
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-312-3878-5
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CITY: Hackensack
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Best Local Similarity
Matches 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 VAVEPFGNPIHN------NTMIMRRSVIDGGL----RFDPAYIHA---EDY---KF 196
                                                                                                                                                      4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GOSCASCHLICH, EMIL C.

TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF

TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

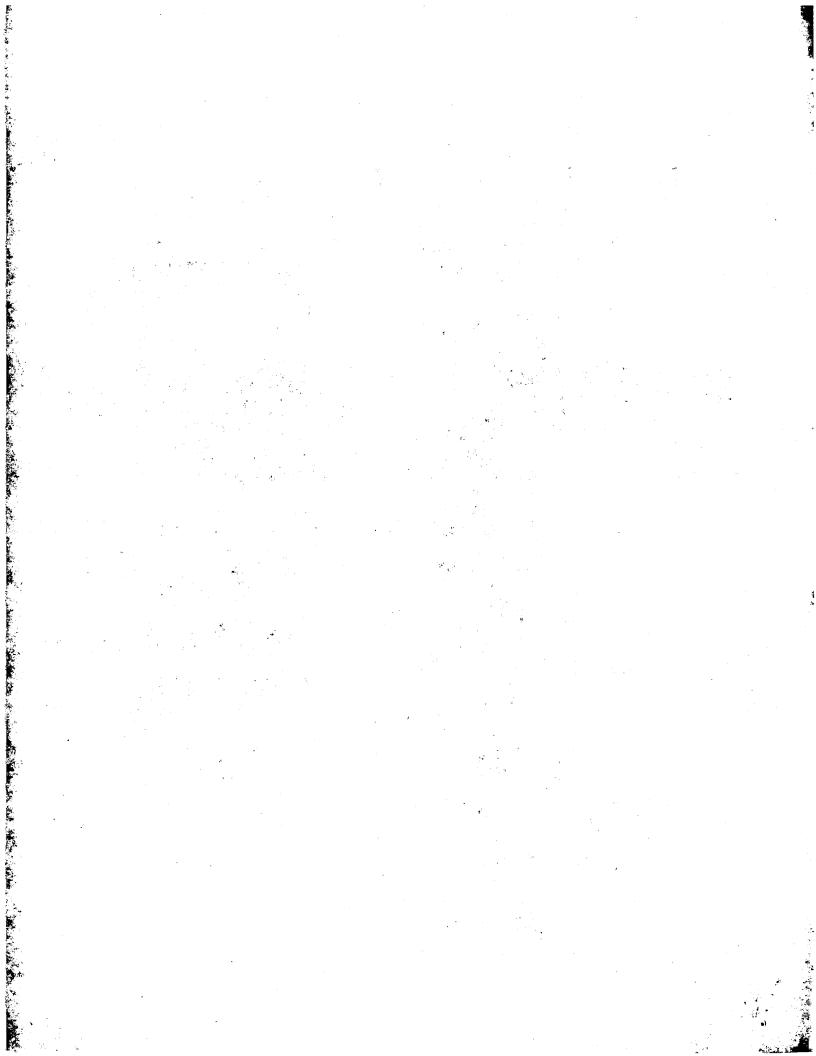
STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey
  Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,426
     DB 1;
11.1%; Score 176.5; DB 1
22.6%; Pred. No. 1.6e-08;
Live 60; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : : |: |: |: |: | 197 | 198 | 1997 WYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQ 230
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REGISTRATION NUMBER: 26,742
REFERNCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYEE Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 536
PLOR PPPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
FILING DATE: September 26, 1994
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13;
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                                                                                                                                                                                                                                                                                                               64 LNEENIGLASSLN----KAVKISKGEYIFRMDADDISYPSRFDKQIRFME-ENSLDFSAT 118
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                  4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                              Query Match 11.1%; Score 176.5; DB 1; Length 337; Best Local Similarity 22.6%; Pred. No. 1.6e-08; Matches 62; Conservative 60; Mismatches 93; Indels 59;
                                                                                                                                                                                                                                                                                                                                              ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-683-426-5
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Search completed: July 31, 2002, 18:56:22 Job time: 353 sec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 31, 2002, 18:50:19 ; Search time 30.44 Seconds (without alignments) 1142.119 Million cell updates/sec Run on:

US-09-900-038A-1 1590

1 MNYSIIMSVYNEPLNYVRDS......LINDINILVLKLFGGEKQSD 313 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 segs, 111073796 residues Searched:

Potal number of hits satisfying chosen parameters:

747574

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

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/SIDSI/gcgdata/hold-geneseq/genesegp-embl/AA1990 DAT:*
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/SIDSI/gcgdata/hold-geneseq/genesegp-embl/AA1997 DAT:* /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
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/SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1985.DAT:*
/SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1985.DAT:*
/SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1987.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Description	Enzyme EPSH involv	Amino acid sequenc	C glutamicum prote	Campylobacter jeju	Amino acid sequenc	Enterococcus faeca	Enterococcus faeca	Cps9G protein whic	Sugar transferase	N. qonorrhoeae qly	Neisseria polyglyc
SUMMARIES	AAY54093	AAY43795	AAG90151	AAY97206	AAY68985	AAU33454	AAU34918	AAY68980	AAW88312	AAR91311	AAW06576
DB	21	21	22	21	21	22	22	21	20	17	18
% Query Match Length DB ID	268	268	274	301	209	106	715	269	260	348	348
% Query Match	17.1	17.1	15.1	14.7	14.0	13.6	13.6	13.5	13.4	13.2	13.2
Score	272	272	240.5	234	223	216	216	214	213	210.5	210.5
Result No.	п	7	e	4	S	9	7	œ	σ	10	11

Germond JE, Lamothe G;

Stingele F,

(NEST) SOC PROD NESTLE SA

AAY68974 Cosli protein which			AAY54095 Enzyme EPSJ involv	AAY43797 Amino acid sequenc	7	0	AAB47427 EpsM. Lactococcus	AAY97213 Campylobacter jeju	AAR91314 N. gonorrhoeae qly	Lipo-oliqosacci		AAY96212 P. multocida hya	G,	AAY43099 P. multocida hyalu			0	9	9	80	4	AAY81720 Streptococcus pneu	AAW61236 Streptococcus pneu	EpsN.	0 Enzyme	2 Amino	5 Cps1J p	1 Enzyme	73 Amino acid s	8 Novel human	Novel human	
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21		22																				21										
322	270	298	327	327	332	345	329	302	337	337	277	702	972	972	334	336	336	965	278	324	324	328	. 281	332	330	330	322	322	322	973	973	973
	12.6						11.5	11.4	11.1	11.1	10.6	10.6	10.4	10.4	10.4	10.4	10.4	10.4	10.3	10.1	10.1	10.1	10.1	10.0	10.0	10.0	6.6	8.6	8.6	9.4	9.4	9.4
0	200	198	193.5	193.5	187	186.5	182.5	180.5	176.5	176.5	168	168	9	165.5	165	165	165	165	164	161	161	161	160	2	158.5	28	22	156.5	26	150	150	120
210																																

ALIGNMENTS

Exopolysaccharide; EPS; ESP enzyme; EPSA; EPSB; EPSB; EPSE; EPSF; EPSG: EPSH: EPSI: EPSJ: EPSK: Lactobacillus delbrueckii buigaricus; activated D-galactose pyranose, saccharide, beta-glycosyltransferase; transcription attenuator; glucosyl-phospho-transferase; alpha-glycosyltransferase; glucosyltransferase; EPSL; EPSM; alpha-glycosyltransferase; EPS Dolymerase; glycosyltransferase; EPS Dolymerase; glycosyltransferase; EPSN; phosphofuranose; transporter; food; fermented milk product; yoghurt; cheese; flavour stability; organoleptic property. Enzyme EPSH involved in exopolysaccharide blosynthesis. Lactobacillus delbrueckii bulgaricus. AA. AAY54093 standard; Protein; 268 98EP-0201310. 98EP-0201311. 98EP-0201312. 99WO-EP02841. (first entry) 22-APR-1998; 22-APR-1998; 22-APR-1998; WO9962316-A2 22-APR-1999; 27-MAR-2000 09-DEC-1999 AAY54093; Н AAY54093 RESULT THE STATE OF THE S us-09-900-038a-1.rag

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                                                                                                                                                             expoplysaccharides (EPS). These energy are designated EPSA-EPSN, and are encoded by open reading frames epsA-epsN. The enzymes are isolated are encoded by open reading frames epsA-epsN. The enzymes are isolated from Lactobacillus delbrueckii bulgaricus. The proteins are used in a method for the synthesis of EPS, which includes at least one step of forming a bond (alpha or beta-isomer) between C-1 (carrying the ceducing aldebyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar unit, present at the end of a chain of sugar residues bonded to the primer. EPSA is attenuator of transcription which influences from the control of the molecular weight and/or the length of the could involved in the control of the molecular weight and/or the length of the could be EPSD. EPSL and EPSM are involved in synthesis of EPSE is a glactosy- or glucosyl-phospho-transferase which catalyses the transfer of the first saccharide on the primer; EPSF and EPSR is calpha-glycosyltransferases; EPSG as a glucosyltransferase; EPSK is calpha-glycosyltransferases; EPSG is a glucosyltransferase; EPSK is cresponsible for the polymerisation of the repetitive units; and EPSN is responsible for export of the EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoghurt can debse. e.g. their organoleptic properties and flavour stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KILLNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEEN-SLDFSATL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 IELIDQKGNLVY---KQRESNKIYLINDIRKMLLNRSILAHPTWCVKKKVFDKLMGYR-- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 -DLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SIIMSVYNEPLNY--VRDSVESILNQTLTDFEFIIVID-NPSRGDLKQFLTEYSVVDNRI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eps operon; Lactobacillus delbrueckii bulgaricus Lfi5; enzyme; epsA;
                                             new recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties of fermented milk products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of epsH of L. delbrueckii bulgaricus Lfi5.
                                                                                                                                                    AAY54086-99 represent enzymes involved in the biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 272; DB 21;
Pred. No. 5.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 fksfgmltkgipyiikpiliglipqkifyiirknry 268
                                                                                                                      Claim 13; Page 154-155; 162pp; French.
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              2000-097267/08
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                               N-PSDB; AAZ54260
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by the eps operon of Lactobacillus delbrueckii bulgaricus Lifs. The oper ocottains 14 open reading frames, and encodes enzymes (epsh, epsp, epsp
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epsB; epsC; epsD; epsE; epsF; epsG; epsH; epsI; epsK; epsK; epsL; epsm; exopolysaccharide biosynthesis; EpS; intersugar bond; antitumour; probiotic; foodstuff; organoleptic quality; flavour; lactic acid bacteria; acidified milk product; yoghurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant enzymes for biosynthesis of exopolysaccharides having e.g. antitumor or probiotic properties or useful in fermented milk products.
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                                                                                                                                                                                                                                                 Lactobacillus delbrueckii bulgaricus
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98EP-0201312.
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                                                                                                                                                                                                                                                                                                                                                    W09954475-A2
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22-APR-1998;
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Best Local Si
Matches 82;
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188

AAY97206 standard; Protein; 301

130 if...gqsadlptsqdirqillvknpiihssvmyrkqvveqiggyslemtrsqdyelflr 186 ----GALADFKIGLLNKVLLQYRLNENGIS-QTNKFKQYIYSAILQDFYKEKSYIDITKI 242

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ochiai K, Yokoi H;
                                                                                                                                                                                                                                                          Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 274;
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Pred. No. 4.5e-14;
2; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                        C glutamicum protein fragment SEQ ID NO: 3905
                                              AAG90151 standard; Protein; 274 AA.
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26.2%; Pred
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Senoh A, Ikeda M,
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2000; 2000EP-0127688.
                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum.
                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              EP1108790-A2
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07-APR-2000;
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Local Sim.
71;
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Tatelshi N,
                                                                                                                                                    26-SEP-2001
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                                                                                                   AAG90151;
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Matches
                      AAG90151
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are useful for synthesising simplyated oligosaccharides such as ganglioside, lysoganglioside or their mimics. Glycosyltransferases are useful for chemo-enzymatic synthesis of oligosaccharides, including gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimics, such as C. jejuni and the concleic acids are used as probes to study expression of genes involved in ganglioside mimetic synthesis. Antibodies raised against the glycosyltransferases are also useful for analyzing the cucleic acids are also useful for designing antisense oligonucleotides for inhibiting expression of the Campylobacter concleic acids are also useful for designing antisense oligonucleotides for inhibiting expression of the Campylobacter carges that are involved in the biosynthesis of ganglioside mimics that can mask the pathogens from the host's immune system. The oligosaccharides are useful as dlagnosing reagents or as therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel glycosyltransferase polypeptides and polynucleotides useful for biosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
                                                                                                                                                                                            acetyltransferase; glycosyltransferase; Beta-1,4-GalNAc transferase; Beta-1,3-galactosyltransferase; alpha-2,3-sialyltransferase; sialic acid synthase; CMP-sialic acid synthetase; mimic; antibody; immunogen; ganglioside.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A reaction mixture for the synthesis of a sialylated oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and as immunogens for producing antibodies. Bacterial glycosyltransferase can be used to catalyse the formation of ollosaccharides that are identical to the corresponding mammalian structures and are easier and less expensive to produce in large quantity, compared to the mammalian glycosyltransferase. The
                                                                                                                               Campylobacter jejuni OH4384 Beta-1,3-galactosyltransferase.
                                                                                                                                                                       Biosynthetic locus; biosynthesis; lipid A biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 102-103; 120pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CANA ) NAT RES COUNCIL CANADA.
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31-JAN-2000; 2000US-0495406.
                                                                                                                                                                                                                                                                                                                Campylobacter jejuni OH4384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2000; 2000WO-CA00086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA53723, AAA53720.
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wakarchuk WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-524418/47
                                                                                                                                                                                                                                                                                                                                                          WO200046379-A1.
                                                                                   22-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gilbert M,
                                       AAY97206;
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10;

27;

Conservative

70 GLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENS-LDFSATLIELIDQKGN 128

17 yde---ycsqsiksvceqnyenwqivlvldgapikdvpqwvkeh----erikiveqkirq 69 YNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKILLNEENI 69

g

ð a 129 LVYKORESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYR-DLVPVEDYDFAIR 187

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Disclosure; Fig 6; 144pp; English.
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N-PSDB; AAS51313.
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
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16-FEB-2001;
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQKGNLVYKQRESNK-IYLTNDIRKMLLNRSILAHPTW--CVKKKVFDKLMGYRDLVPVE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .172 ---fas1rlekdvkinmaedvilyypm----lsqaqkia--ymncnlyhyvpnnnsicnt 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K----ITNYFOEYVIKKRYTQQE--LSKYFELKSTPSITIR-KLYICLYLYFKSPLVRRL 293
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capsular gene cluster; serotype 7; polysaccharide biosynthesis; capsular component; antigen; regulation; chain length determination; complement-mediated opsonophagocytosis; serotype-specific detection; antigen; vaccine; Streptococcal disease; Cps7E; Cps7E; Cps7G;
bacterial origin of the enzymes facilitates expression of large quantities of the enzymes using relatively inexpensive prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 DYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYSAILQDFYKEKSYIDIT
                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                    Length 301;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of Cps7H of a capsular gene cluster.
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                                                                                                                                                                                                                                                                                14.7%; Score 234; DB 21; 28.2%; Pred. No. 2.1e-13;
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY68985 standard; Protein; 209 AA.
                                                                                                                                                                                                                                                                                                                                                                  53;
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280 lak-iniltlki 290
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                                                                                          expression systems.
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                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                301 AA;
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The proteins AAY68982-85 are encoded by the capsular gene cluster of Streptococcus suis serotype 7. The genes in this cluster are involved in polysacoharide biosynthesis of capsular components and antigens. The capsule confers bacterium resistance to complement-mediated opsonophagocytosis. The gene cluster is used as a source of probes and primers for serotype-specific detection of S. suis and is also useful for recombinant production of the proteins. The proteins are then useful for producing antigens that can be used in vaccines, for controlling or eradicating a Streptococcal disease, in humans or animals, e.g. against S. suis in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 DOKGNLVYKORESNKIYLTND---IRKMLLNRSILAHPTWCVKKKVFDKLMGYRDLVPVE 180
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Pred. No. 1.3e-12;
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29.0%; Pre
tive 53;
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2000US-27727P.
2000US-242578P.
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2000US-253625P.
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Xu HH;
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Best Local Similarity
Matches 62; Conserv
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WO200170955-A2.
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                                                                      The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets in antibiotic development. The antisense nucleic acids can also be used to invention antibiodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
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            New polynucleotides for the identification and development of antiblotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                               Length 706;
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                                                  Example 3; Seq ID No 4950; 511pp; English.
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Best Local Similarity
Matches 79; Conserv
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibloitics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruqianosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets in antibiotic development. The antisense nucleic acids can also be used to dentify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

The sequence data for this patent did not form part of the discovery of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                          Carr GJ;
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                                                                                                                                                                                                                                                                                                                                                                                   Trawick JD,
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Xu HH;
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2000US-253625P.
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21-MAR-2001; 2001WO-US09180
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22-DEC-2000;
16-FEB-2001;
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                                                                                                 170 ggyqtlpyvedyflwvrmiasgskfanidetlvlarvg-ngmfnrrgnreqinswtllie
   LDFSATLIELIDQKGNLVYKQRESNKIYLT - - NDIRKMLLNRSILAHPTWCVKKKVFDKL
                                                                                                                                      FYKEKSYIDITKITNYFQEYVIKKRYTQQELSKYFELKSTP-SITIRKLYICLYLYFKSP
                                                                     MGYRDLVPVEDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIYS-AILQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food faeces or patient samples
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sugar transferase involved in 0157 antigen biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen; 0157 antigen; sugar transferase; wbdN gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 213; DB 20;
llarity 27.2%; Pred. No. 1.5e-11;
Conservative 54; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haemorrhagic colitis; diagnosis
                                                                                                                                                                                                                                                                                                                         AAW88312 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 8; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97AU-0008162.
97AU-0006545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-AU00315
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-059669/05.
                                                                                                                                                                                                                                     257 wikkliygki 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                        289 LVRRLLINDI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX06749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09850531-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                        26-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diarrhoea;
                                                                                                                                                                                                                                                                                                                                                        AAW88312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                    230
                                                                                                                                                                       229
                                 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The proteins AAV68977-81 are encoded by the capsular gene cluster of Streptococcus suis serotype 9. The genes in this cluster are involved in polygaccharide biosynthesis of capsular components and antigens. The proteins have glycosyltransferase activities (Cps9E, Cps9F) and unknown functions (Cps9D, CpsG, Cps9H). The capsule confers bacterium resistance to complement-mediated opsonophagocytosis. The gene cluster is used as a source of probes and primers for serotype-specific detection of S. suis and is also useful for production of the proteins. The proteins are then useful for producing antigens that can be used in vaccines, for controlling or eradicating a Streptococcal disease, in humans or animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or mutants for vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKILLINEENIGLASSLNKAVKISKGE-----YIFRMDADDISYPSRFDKQIRFMEEN-S 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : |:| || :|| :|| :|| 61 ffktialeknsglgialneglkhcnyewvctkwilmm----lhihtrfekqvnfikqnpt 116
                                                                                                                                                                                                                                                   Capsular gene cluster; serotype 9; polysaccharide biosynthesis; capsular component; antigen; regulation; chain length determination; complement-mediated opsonophagocytosis; serotype-specific detection; antigen; vaccine; Streptococcal disease; Cps9D; Cps9E; Cps9F; Cps9G; CpsPH; glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNYSIIMSVY-NEPLNYVRDSVESIL-NQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.5%; Score 214; DB 21; 25.5%; Pred. No. 1.2e-11; iive 63; Mismatches 112;
262 KYFELKSTPSITIRKLYICLYLYFKSPLVRRLLINDINI 300
                      Cps9G protein which has an unknown function.
                                                                                                                  AAY68980 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 5; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. against S. suis in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-NL00460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98EP-0202465.
                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-195104/17.
                                                                                                                                                                                                                                                                                                                                                        Streptococcus suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ60931
                                                                                                                                                                                                                                                                                                                                                                                      WO200005378-A2.
                                                                                                                                                                                     30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith HE;
                                                                                                                                                    AAY68980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                 AAY68980
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11;

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Length 348;

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Query Match
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                                                                                      DOKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKK----KVFDKLMGYRDLVPV 179
                                                                                                                                               180 EDYDFAIRGALADFKIGLLNKVLLQYRLNENGISQTNKFK--QYIYSAILQDFYKEKSYI 237
                                                                                                                                                                                                           63
                               5 Glycosyltransferases (AAR91311-15) are products of the lgt locus (AAT44061) of Neiserria gonorrhoeae strain F62. Glycosyltransferase LgtA (AAR91311) can be obtd. by expression of the lgtA coding sequence in recombinant host cells. A method for adding GalNAc or GloNAc betal-3 to Gal comprises contacting a reaction mixture confg activated GalNAc or GloNac to an acceptor moiety comprising a Gal residue in the presence of LgtA. Oligosaccharides can be produced that, when attached to non-toxic lipids, are useful for Neisseria waccine prepr. Blood group core oligosaccharides, and mimics of lacto-N-neotetranse, gangliosides and saccharide portions of globoglycolipids can also be produced using the enzymes.
                                                                      LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATLIELI
            SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding glycosyl transferase(s) – used in the diagnosis of infection with Neisseria and for the blosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycosyltransferase; lipo-oligosaccharide; lgt gene; LOS locus;

    N. gonorrhoeae glycosyltransferase LgtA.

                                                                                                                                                                                                                                                     238 DITKITNYFQEYV --- IKKRYTQQELSK 262
                                                                                                                                                                                                                                                                                 228 sfpktlyyfllyasngvmkkithsllrr 255
                                                                                                                                                                                                                                                                                                                                                           AAR91311 standard; Protein; 348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria gonorrhoeae strain F62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Fig 2b; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0312387.
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                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-200924/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligo:saccharide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT14061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gotschlich EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9610086-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                        AAR91311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                              124
                                                                                                                                                                                                                                                                                                                                             AAR9131
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15;
                                                                                                                                               SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                                                                                                                               235 -eiaggigk-----tarndflgsmgfktrfdsleyrqtkaaayelpekdlpeedfera 286
                                                                                                                              LNEENIGLASSLNKAV-KISK-----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
                                                                                                                                                                                                                                                            MGY----RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY 223
                                                                                                                                                                                                                                                                           Gaps
                                                                                4 SIIMSVYNEPLNYVRDSVESILNOTLTDFEFIIVIDNPSRGDLKOFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transfer of at least 2 saccharide units using poly:glycosyl:transferase - isolated from N. gonorrhoeae, catalyses the addition of both GlcNac and GalNac di:saccharide(s) units to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A novel polyglycosyltransferase (PGTase) (AAW06576) from Neisseria gonorrhoeae ATCC 33084 catalyses the stereospecific conjugation of 2 specific activated saccharide units (e.g. UDP-GICNAC, UDP-GAINAC, UDP-GAI) to specific acceptors having a galactose moiety at a non-reducing end. It is the first PGTase reported to be capable of transfer of more than one different saccharide moiety. The PGTase is encoded by nucleotides 445-1488 of a lipo-oligosaccharide gene
                                                                                                                                                                                                                                                                                                                           SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT - - - QQELSKYFEL - - KSTPSITIRKL
                                 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polyglycosyltransferase; N-acetylglucosaminyl transferase; N-acetylgalactosaminyl transferase; lipo-oligosaccharide.
               3.8e-11
                                Mismatches
13.2%; Score 210.5; 27.8%; Pred. No. 3.86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW06576 standard; Protein; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria polyglycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roth S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria gonorrhoeae ATCC 33084
                                55;
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                                Conservative
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             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         287 rrflyqcfk 295
                                                                                                                                                                                                                                                                                                                                                                                           278 YICLYLYFK 286
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                                86;
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                  Local
                Best Loc
Matches
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22-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       It can be produced in transformed host cells and used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 LNEENIGLASSLNKAV-KISK-----GEYIFRMDADDISYPSRFDKQIRFMEENS--LDF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 -eiaggigk-----tarndflgsmgfktrfdsleyrgtkaaayelpekdlpeedfera 286
                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 MGY---RDLVPVEDYDF----AIRGALADFKIGLLNKVLLQYRLNENGISQTNKFKQYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAILQDFYKEKSYIDITKITNYFQEYVIKKRYT----QQELSKYFEL--KSTPSITIRKL
                                                                                                                                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                                         Length 348;
                                                                                                                                                                                                                                                    13.2%; Score 210.5; DB 18; Length 27.8%; Pred. No. 3.8e-11; ive 55; Mismatches 123; Indels
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98EP-0202467.
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Best Local Similarity
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                                                                                                                            348 AA;
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22-JUL-1998;
(AAT49230).
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16;
                                                                                                                                            The proteins AAY68970-76 are encoded by the capsular gene cluster of Streptococcus suis serotype 1. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins have glycosyltransferase activities (CpsIE, CpsIG, CpsII, CpsIJ, CpsIJ, and CP polymerase activities (CpsIH). The capsule confers bacterium resistance to complement mediated opsonophagocytosis. The gene cluster is used as a source of probes and primers for serotype-specific detection of S. suis and is also useful for recombinant production of the proteins. The proteins are then useful for producing antigens that can be used in vaccines, for controlling or eradicating a Streptococcal disease, in humans or animals, e.g. against S. suis in pigs.
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Disclosure; Fig 4; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunity; immunogen; ganglioside.
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31-JAN-2000; 2000US-0495406
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Best Local Similarity 25.1%
Matches 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                 is useful for synthesising sialylated oligosaccharide construct minnature in the synthesising sialylated oligosaccharide such as ganglioside, lysoganglioside or their minics. Glycosyltransferases of ganglioside, lysogangliosides and other oligosaccharides, that have constituted for chemo-enzymatic synthesis of oligosaccharides, including gangliosides and other oligosaccharides that have bological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms of that synthesize ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes or nucleic acids are used in ganglioside mimetic synthesis. Antibodies raised against the glycosyltransferases are also useful for analyzing the expression patterns of these genes involved in pathogenesis. The cultion patterns of these genes involved in pathogenesis. The outleic acids are also useful for designing antisense oligonucleotides for inhibiting expression of the campylobacter concludes that are involved in the biosynthesis of ganglioside mimics of that can mask the pathogens from the host's immune system. The coligosaccharides are useful as diagnosing reagents or as therapeutics and as immunogens for producing antibodies. Bacterial coligosaccharides that are identical to the corresponding mammalian structures and are easier and less expensive to produce in large clantical coligosaccharides that are identical to the corresponding mammalian structures and are easier and less expensive to produce in large duantity compared to the mammalian glycosyltransferase. The cantended origin of the enzymes facilitates expression of large expression systems.
                                                                                                                                                                                            Novel glycosyltransferase polypeptides and polynucleotides useful for blosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 lnygedvlfcyiyfmfcekiavfktciyhyefnpng-ryenknkeiln----qnyhdkkk 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||::| ::: :::| :||||| | | |::||: |: | |||| | 5 slipplfns-cdfisralgscinqtlkdle-iliiddkskdnslnmvlefakkdprikif 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIIMSVYNEPLNYVRDSVESILNOTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                                                                                                                                                                                                                                                                                              reaction mixture for the synthesis of a stalylated oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.6%; Score 200; DB 21; Length 270; 26.8%; Pred. No. 2.5e-10; Live 52; Mismatches 119; Indels 2
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                       (CANA ) NAT RES COUNCIL CANADA.
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                                                                        Gilbert M, Wakarchuk WW;
                                                                                                                   WPI; 2000-524418/47.
N-PSDB; AAA53720.
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Best Local S:
Matches 73,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 LIDQKGNLVYKQRESNKIYLTNDIRKMLLNRSILAHPTWCVKKKVFDKLMGYRD--LVPV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 LNEENIGLASSLNKAVKISKGEYIFRMDADDISYPSRFDKQIRFMEENSLDFSATL--IE 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
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                                          Putative glycosyltransferase, involved in cell wall biogenesis #1.
                                                                                                                                                                                                                                                                                                                                                             New nucleotide sequences isolated from Pyrococcus abyssi encode
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                                                                     Hyperthermophilic archaeon; hyperthermophilic protein.
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                                                                                                                                                                                                                                                                                     Thierry JC, Prieur D, Dietrich J, Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 198; DB 22;
Pred. No. 4.3e-10;
0; Mismatches 95;
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27.8%;
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            29-OCT-2001 (first entry)
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Best Local Similarity
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                                                                                                 Pyrococcus abyssi
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Querellou J,
                                                                                                                                                                                                               21-APR-1999;
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                                                                                                                                                                                    21-APR-1999;
                                                                                                                                                        27-OCT-2000.
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59 kv-vhkqngglssarnagmkvatgeyisfidsddylasnmyehvfsimkkecadivvvgr 117

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ANY AAY54086-99 represent enzymes involved in the biosynthesis of exopolysaccharides (EPS). These enzymes are designated EPSA-EPSN, and are encoded by open reading frames epsA-epsN. The enzymes are isolated from Lactchacillus delbrueckii bulgaricus. The proteins are used from Lactchacillus delbrueckii bulgaricus. The proteins are used of forming a bond (alpha or beta-isomer) between C-1 (carrying the ceducing aldehyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar on L., present at the end of a chain of sugar residues bonded to the primer. EPSA is attenuator of transcription which influences control of the molecular weight and/or the length of the polysaccharide; EPSD, EPSL and EPSM are involved in synthesis of EPS; is involved in the control of the molecular weight and/or the length of the colysaccharide; EPSD, EPSL and EPSM are involved in synthesis of EPS; EPSE is a glactosy- or glucosyl-phospho-transferase which catalyses the transfer of the first saccharide on the primer; EPSF and EPSK is calpha-glycosyltransferases; EPSK is a glucosyltransferase; EPSK is capparable for the polymerisation of the repetitive units; and EPSN is responsible for the polymerisation of the repetitive units; and EPSN is responsible for sport of the EPS. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoghurt and cheese, e.g. their organoleptic properties and flavour stability.
                                               ESP enzyme; EPSA; EPSB; EPSB; EPSD; EPSE; EPSF;
                                                                 BPSG; EPSH; EPSI; EPSI; EPSK; Lactobacillus deibrueckii bulgaricus; activated D-galactose pyranose; saccharide; beta-glycosyltransferase; transcription attenuator; glucosyl-phospho-transferase; alpha-glycosyltransferase; glucosyltransferase; EPS polymerase; glycosyltransferase; EPS polymerase; glycosyltransferase; EPS polymerase; glycosyltransferase; EPS polymerase; glycosyltransferase; EPSN; phosphofuranose; transporter; food; fermented milk product; yoghurt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties of
Enzyme EPSJ involved in exopolysaccharide biosynthesis.
                                                                                                                                                                                                                   cheese; flavour stability; organoleptic property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 18; Page 156-157; 162pp; French
                                                                                                                                                                                                                                                             Lactobacillus delbrueckii bulgaricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lamothe G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             98EP-0201310
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98EP-0201312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fermented milk products
                                               Exopolysaccharide; EPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-097267/08.
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22-APR-1998;
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15;

73;

Mismatches 121;

55;

Conservative

83;

g ò

Similarity

Query Match Best Local S: Matches 83;

327 AA;

Sequence

Score 193.5; DB 2. Pred. No. 1.3e-09;

12.2%; 25.0%;

DB 21; Length 327; Indels

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ELIDQKGNLVYKQRESNKIYLTNDIRK - - MLLNRSILAHPTWCVKKKVFDKLMGYRDLVP 178
                                                            234
                                                         179 VEDYDFAIRGALADFKIGLLNKVLL-QYRLNENGISQTNKF---KQYIYSAILQDFYKEK
                                                                                                                        --SYIDITKITNYFQEYV-----IKKR---YTQQELSKYF----ELKSTPSITI
                                                                                         160 wdkv-----ykrslfndvsypegklsedwyttykvfakanrivydstpmyyyrgr
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